

REFERENCE

AUTHORS

Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Phlebotomina: Muscomorpha: Ephyridiidae: Ephyridiinae: Phlebotomina
 1 (bases 1 to 40)
 Liao, G.-C., Rehm, E.J. and Rubin, G.M.
 Insertion site preferences of the P transposable element in *Drosophila melanogaster*
 Proc. Natl. Acad. Sci. U.S.A. 97 (7): 3347-3351 (2000)

JOURNAL
MEDLINE
COMMENT

Contract: Gerald Rubin
 Berkeley Drosophila Genome Project
 University of California, Berkeley
 USA Building, Berkeley, CA 94720-3200, USA
 Fax: 5106439947
 Email: gerry@cellbio.berkeley.edu

Sequence recovery method was inverse PCR

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 001 in the 40 bases. This insertion position refers to the first base of the 9 base target recognition sequence.

Class: transposon-tagged

FEATURES

source

Location/Qualifiers

1..40

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone_lib="Drosophila melanogaster EP line"

/note="Inverse PCR was performed on *Drosophila*

melanogaster strains each of which contains a single EP

transposable element insertion. (The denaturation of these

insertion strains is described in Rehm, E.J., Rubin, G.M., Liao, G.-C.,

A. Laverdy, T., Rehm, E.J., Rubin, G.M., Weigmann, K., Milon, M., Benes

V., Ansoy, W., Cohen, S.M., 1998, Systematic gain-of-function

genetics in *Drosophila*. Development 124:1057-1067.) The

resultant fragment for each strain was directly sequenced

to determine the genomic sequence at the site of

insertion. Details of the protocols used can be found at

<http://fruitfly.berkeley.edu/ep-line/ep-line.html>."

BASE COUNT

7 a 13 c 12 g 8 t

ORIGIN

Query Match

23.8% Score 10; OP 17; Length 40;

Best Local Similarity 100.0%; Pled. No. 9e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGTTGACCAT 17

PB 35 CGTTGACCAT 26

RESULT 10
BH639055
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BH639055 40 bp DNA linear GSS 14-DEC-2002
 109802/AT111E111008 - Kusecuka Grid 1 7aa may's genome, DNA
 sequence
 BH639055
 BH639055 1 G111008112
 GSS.
 Zea mays.
 Zea mays.
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
 Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
 Panicoideae, Andropogoneae, Zea.
 1 (bases 1 to 40)
 Walbot, V.
 Maize genome sequences found using engineered RescueMu transposon
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 725 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 plate: 1008027 row: 6
 Class: transposon-tagged

FEATURES

source

Location/Qualifiers

1..40

/organism="Zea mays"

/db_xref="taxon:4577"

/clone_lib="Zea mays - Kusecuka Grid 1"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/note="Origin: leaf; Vector: Kusecuka (engineered from

phagescript backbone); Site: BamHI; Site 2: BglII;

Kusecuka is a 1.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site www.zmmb.iastate.edu and follow the links for

'RescueMu.' Grid 1 was grown at Berkeley in 2001. DNA was

extracted from leaf punches, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B

cells were transformed and then screened on LB plates with

ampicillin."

BASE COUNT

12 a 5 c 14 g 9 t

ORIGIN

Query Match

23.8% Score 10; PR 17; Length 40;

Best Local Similarity 100.0%; Pled. No. 9e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCGGAGTCAA 36

PB 2 TCGGAGTCAA 11

RESULT 11
TA115C11P

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

TA115C11P 40 bp DNA linear GSS 13-DEC-2000
 T1: brucei shared genomic DNA clone 115c11, forward sequence,
 genomic survey sequence.
 AL462927
 AL462927.1 G111832508
 GSS.
 Trypanosoma brucei.
 Trypanosoma brucei.
 Eukaryota, Eukaryota: Kinetoplastida: Trypanosomatidae:
 Trypanosoma.
 1 (bases 1 to 40)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Greenwood, D., Harris, B., El-Sayed, N., Hou, L.,
 Metcalfe, S.P., Rajandram, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, e-mail: barrell@sanger.ac.uk and
 nhsander@sanger.ac.uk
 constructed at the Institute for Genomic Research (JIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 trypanosoma brucei (7ppmu974) (974) was mechanically sheared
 to give a light size distribution (4 kb). The v + 1 method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Baking small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999)
 Email: nhsander@jigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at <http://www.sanger.ac.uk/genomes/TSB/brucei/>.

FEATURES Location: 2931151000
 SOURCE 1..40
 ORGANISM "Trypanosoma brucei"
 /stratn "TRE927"
 /db_xref "taxon:5601"
 /clone "115c11"
 BASE COUNT 7 a 11 c 12 g 10 t
 ORIGIN

Query Match 24.8% Score 10; DB 17; Length 40;
 Post local similarity 100.0%; Prod. No. 9,1e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CV 21 GATGAGTACG 40
 DB 26 TGAAGTTCAG 45

RESULT 12
 REF784672 41 bp mRNA linear EST 12 JAN 2001
 LOCUS 65211130811 RefSeq:K114 Kozak consensus (Kozak 1986) IMAGC1429300
 DEFINITION 5' mRNA sequence.
 ACCESSION Ref784672 GI:1289738
 VERSION Ref784672.1 GI:1289738
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 41)
 REF 1 McEwen, J. et al. 1997.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: eapops@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The M.A.G.E. Consortium (LMNC)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the M.A.G.E. Consortium/LMNC at:
 http://lmnc.nih.gov
 Plasmid: IMAGC52 row: 1 column: 01
 High quality sequence stop: 47.
 Location/Qualifiers
 1..41
 ORGANISM "Mus musculus"
 /stratn "EVH/2"
 /db_xref "taxon:10090"
 /clone "IMAGC:429300"
 /clone_1lb="N1_GCAP_Kid14"
 /lab_host "DH10B (TL Plaque-Resistant)"
 /note="Organism: Kidney; Vector: pCMV-Sport6; Site: 1; Note:
 Site 2: Salt cloned unidirectionally, primer oligo dT.
 Average insert size: 177 bp. Constructed by J.E.
 Technologies. Note: this is a NCI/NCAP library." 1

BASE COUNT 7 a 10 c 20 g 4 t
 ORIGIN

Query Match 24.8% Score 10; DB 12; Length 41;
 Post local similarity 100.0%; Prod. No. 9,1e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CV 25 GATGAGTACG 44
 DB 20 GATGAGTACG 29

RESULT 13
 AA994992 43 bp mRNA linear EST 27 AUG 1998
 LOCUS 659609.31 Sources: RefSeq:K114 Homo sapiens cDNA clone
 DEFINITION

EMBL:U25757.2 Similar to: U54375 (GenBank) 25 AUG 1998
 Sequence:
 AA994992 GI:8181401
 VERSION AA994992.1 GI:8181401
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 43)
 REF 1 GATGAGTACG 44 Site 2: No gap.
 2 1 GATGAGTACG 44 Site 3: No gap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: eapops@mail.nih.gov
 This clone is available royalty free through LMNC. Contact the
 IMAGC Consortium (Info@imc.nih.gov) for further information.
 Insert Length: 434. Std Error: 0.50
 Seq primer: 40m3 1wd. El from Ambisham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..43
 ORGANISM "Homo sapiens"
 /stratn "14201:9406"
 /clone "IMAGC:162752"
 /clone_1lb "Sources: NCI, J.Gibbs"
 /lab_host "DH10B"
 /note="Organism: Kidney; Vector: pCMV-Sport6 (Pharmacia) with
 a modified polylinker; Site: 1; Note: Site 2: No gap;
 Equal amounts of plasmid DNA from three normalised
 libraries (total input band by Toles 3HL, and 6 cell
 NCI/NCAP/GEN) were mixed, and six clones were made in
 vitro. Following MAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The direct
 was PCR amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 75438 728711, and 729096-741899. Subtraction by Beutlo
 Sources and M. Farina banding." 1

BASE COUNT 9 a 9 c 15 g 10 t
 ORIGIN

Query Match 24.8% Score 10; DB 9; Length 43;
 Post local similarity 100.0%; Prod. No. 9,2e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CV 15 GATGAGTACG 24
 DB 14 GATGAGTACG 5

RESULT 14
 BB854287 43 bp DNA linear GSS 13 JUN 2002
 LOCUS BB854287
 DEFINITION BB854287.1 GI:21424178
 ACCESSION BB854287
 VERSION BB854287.1 GI:21424178
 KEYWORDS GSS.
 SOURCE Thai cross.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicot;
 Rosidae; eurosids 1; Brassicales; Brassicaceae; Arabidopsis
 1 (bases 1 to 43)
 REF 1 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Chouk, K., Gauthier,
 J., Jeske, A., Karnos, M., Kim, C.J., Parker, H., Proebst, L., Shinn, P.,
 Zimmermann, J., and Eick, J. R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)

COMMENT

Contact: Joseph P. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 458 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of ATG950960.
Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
1..43
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SAIK_076302.53.45.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/ttn_protocols.html"

BASE COUNT

14 a 9 c 9 g 11 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 10; DB 17; Length 43;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATCGGTGAGC 25

|||||

DB 32 ATCGGTGAGC 41

RESULT 15

BH863967

LOCUS

45 bp DNA linear GSS 05-NOV-2002
SAIK_06605 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SAIK_095005, DNA sequence.

ACCESSION

BH863967.1 GI:22099865

VERSION

KEYWORDS

GSS;

SOURCE

thale cress.
Arabidopsis thaliana
Eubarchy: Viridiplantae; Streptophyta; Embryophyta; Eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 45)

REFERENCE
AUTHORS
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, P., Gadrinab,
C., Jeske, A., Karnes, M., Kim, G.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

TITLE

JOURNAL

COMMENT

Unpublished (2001)
Contract: Joseph P. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of ATG928650.
Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
1..45
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SAIK_095005"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines"

BASE COUNT

each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/ttn_protocols.html"

10 a 10 c 10 g 15 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 10; DB 17; Length 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGTTGAGCAT 17

|||||

DB 31 CGTTGAGCAT 40

Search completed: April 18, 2003, 04:37:01
Job time: 25195 secs

•

•

•

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

GM nucleic - nucleic search, using sw model

Run on: April 17, 2003, 11:32:34 Search time 2046 seconds

(without alignments)
53.038 Million cell updaters/sec

Title: US-09-701-394-1

Perfect score: 42
1 accgatggcttgagcagcagc 42

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Search: 2054610 steps, 14551402978 positions

Word size: 0

Total number of hits satisfying chosen parameters: 84150

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database:

GenEmb1:
1: gb_da:
2: gb_hg:
3: gb_in:
4: gb_cm:
5: gb_ov:
6: gb_pat:
7: gb_pi:
8: gb_pi:
9: gb_pi:
10: gb_pi:
11: gb_pi:
12: gb_pi:
13: gb_pi:
14: gb_pi:
15: gb_pi:
16: gb_pi:
17: gb_pi:
18: gb_pi:
19: gb_pi:
20: gb_pi:
21: gb_pi:
22: gb_pi:
23: gb_pi:
24: gb_pi:
25: gb_pi:
26: gb_pi:
27: gb_pi:
28: gb_pi:
29: gb_pi:
30: gb_pi:
31: gb_pi:
32: gb_pi:
33: gb_pi:
34: gb_pi:
35: gb_pi:
36: gb_pi:
37: gb_pi:
38: gb_pi:
39: gb_pi:
40: gb_pi:
41: gb_pi:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	24	57.1	28	6	AX448933	AX448933 Sequence
C 2	24	57.1	28	6	AX448933	AX448933 Sequence
C 3	24	57.1	28	6	AX448933	AX448933 Sequence
C 4	22	52.4	25	6	AX358457	AX358457 Sequence
5	22	52.4	26	6	AX7384	AX7384 Sequence
6	22	52.4	26	6	AX358457	AX358457 Sequence
7	22	52.4	26	6	AX075383	AX075383 Sequence
8	22	52.4	26	6	AX015219	AX015219 Sequence
9	22	52.4	26	6	AX030701	AX030701 Sequence
10	22	52.4	26	6	AX166503	AX166503 Sequence
11	22	52.4	26	6	AX174821	AX174821 Sequence
12	22	52.4	26	6	AX175502	AX175502 Sequence
13	22	52.4	26	6	AX175510	AX175510 Sequence
14	22	52.4	26	6	AX358457	AX358457 Sequence
15	22	52.4	26	6	AX300719	AX300719 Sequence
16	22	52.4	26	6	AX358457	AX358457 Sequence
17	22	52.4	26	6	AX453697	AX453697 Sequence
18	22	52.4	26	6	AX013215	AX013215 Sequence
19	22	52.4	26	6	AX013215	AX013215 Sequence
20	22	52.4	26	6	AX013215	AX013215 Sequence
21	21	50.0	21	6	AX391927	AX391927 Sequence
22	21	50.0	21	6	AX391927	AX391927 Sequence
23	21	50.0	21	6	AX391927	AX391927 Sequence
24	20	47.6	20	6	AX357810	AX357810 Sequence
25	20	47.6	20	6	AX357810	AX357810 Sequence
26	20	47.6	20	6	AX357810	AX357810 Sequence
27	20	47.6	20	6	AX357810	AX357810 Sequence
28	20	47.6	20	6	AX357810	AX357810 Sequence
29	20	47.6	20	6	AX357810	AX357810 Sequence
30	20	47.6	20	6	AX357810	AX357810 Sequence
31	20	47.6	20	6	AX357810	AX357810 Sequence
32	19	45.2	19	6	AX348117	AX348117 Sequence
33	18	42.9	18	6	AX111622	AX111622 Sequence
34	18	42.9	18	6	AX111622	AX111622 Sequence
35	16	38.1	16	6	AK073032	AK073032 Sequence
36	16	38.1	16	6	AK073032	AK073032 Sequence
37	16	38.1	16	6	AK073032	AK073032 Sequence
38	16	38.1	16	6	AK073032	AK073032 Sequence
39	16	38.1	16	6	AK073032	AK073032 Sequence
40	16	38.1	16	6	AK073032	AK073032 Sequence
41	16	38.1	16	6	AK073032	AK073032 Sequence
42	16	38.1	16	6	AK073032	AK073032 Sequence
43	16	38.1	16	6	AK073032	AK073032 Sequence
44	16	38.1	16	6	AK073032	AK073032 Sequence
45	16	38.1	16	6	AK073032	AK073032 Sequence

ALIGNMENTS

RESULT 1
AX448933/C
Sequence 33 from Parent W0226823.
Accession AX448933
Version AX448933.1 GI:21697801
Keywords
Source
Organism
Reference
Authors
Title
battaglini, P., Feder, J. N., Muller, C., Panatharan, C. S.,
Westphal, K., Bakken, D. R., Caracci, A., Barber, L. and Forrester, M. G.
A novel human g-protein coupled receptor, hupbm7, expressed
highly in spinal cord

Prod. No. is the number of results predicted by chance to have a

JOURNAL: Patent: WO 0226982 A 26 04 APR 2002;
 FEATURES: Bristol-Myers Squibb Co. (US)
 SOURCE: Location/Qualifiers
 1..28
 /organism "synthetic construct"
 /db_xref "taxon:32640"
 /note "GAGHH-PVIC Tagmu(R) Probe"
 BASE COUNT 6 a 11 c 3 q 8 t
 ORIGIN

Query Match 57.1%; Score 24; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 GGTGAAGGTGGAGTCAAGGATT 42
 |||||||
 26 GGTGAAGGTGGAGTCAAGGATT 4

RESULT 2
 LOCUS: AX451589 28 bp DNA linear PAT 03 JUL 2002
 DEFINITION: Sequence 28 from Patent WO0226982.
 ACCESSION: AX451589
 VERSION: AX451589.1 GI:2169858
 KEYWORDS:
 SOURCE: synthetic construct;
 ORGANISM: artificial sequences;
 REFERENCE: 1
 AUTHORS: Foster, J.N., Minier, G., Ramnathan, C.S., Hawken, D.R., Cacace, A., Barber, J., and Kornacker, M.G.
 TITLE: A human protein coupled receptor, haptomye, expressed highly in small intestine
 JOURNAL: Patent: WO 0226982-A 26 04 APR 2002;
 FEATURES: Bristol-Myers Squibb Co. (US)
 SOURCE: Location/Qualifiers
 1..28
 /organism "synthetic construct"
 /db_xref "taxon:32640"

Query Match 57.1%; Score 24; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 GGTGAAGGTGGAGTCAAGGATT 42
 |||||||
 26 GGTGAAGGTGGAGTCAAGGATT 4

RESULT 3
 LOCUS: AX456896 28 bp DNA linear PAT 06 JUL 2002
 DEFINITION: Sequence 28 from Patent WO0226982.
 ACCESSION: AX456896
 VERSION: AX456896.1 GI:21715747
 KEYWORDS:
 SOURCE: synthetic construct;
 ORGANISM: artificial sequences;
 REFERENCE: 1
 AUTHORS: Foster, J.N., Minier, G., Ramnathan, C.S., Hawken, D.R., Cacace, A., Barber, J., and Kornacker, M.G.
 TITLE: A human protein coupled receptor, haptomye, expressed highly in small intestine
 JOURNAL: Patent: WO 0226982-A 26 04 APR 2002;
 FEATURES: Bristol-Myers Squibb Co. (US)
 SOURCE: Location/Qualifiers
 1..28
 /organism "synthetic construct"
 /db_xref "taxon:32640"

BASE COUNT 6 a 11 c 3 q 8 t
 ORIGIN

Query Match 57.1%; Score 24; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 GGTGAAGGTGGAGTCAAGGATT 42
 |||||||
 26 GGTGAAGGTGGAGTCAAGGATT 4

RESULT 4
 LOCUS: AX458457 25 bp DNA linear PAT 14 FEB 2002
 DEFINITION: Sequence 7 from Patent WO0202780.
 ACCESSION: AX458457
 VERSION: AX458457.1 GI:18675071
 KEYWORDS:
 SOURCE: synthetic construct;
 ORGANISM: artificial sequences;
 REFERENCE: 1
 AUTHORS: Scharm, H.
 TITLE: Human serine-threonine kinase
 JOURNAL: Patent: No. 0226982-A 26 04 APR 2002;
 FEATURES: MEK-R PATENT YAMH (DE)
 SOURCE: Location/Qualifiers
 1..25
 /organism "synthetic construct"
 /db_xref "taxon:32640"
 /note "Primer 4"
 BASE COUNT 6 a 4 c 10 q 6 t
 ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

21 TGAAGGTGGAGTCAAGGATT 42
 |||||||
 1 TGAAGGTGGAGTCAAGGATT 22

RESULT 5
 LOCUS: A57484 26 bp DNA linear PAT 03 MAR 1998
 DEFINITION: Sequence 21 from Patent EP0766008.
 ACCESSION: A57484
 VERSION: A57484.1 GI:3712644
 KEYWORDS:
 SOURCE: unidentified;
 ORGANISM: unidentified;
 REFERENCE: 1 (bases 1 to 26)
 AUTHORS: Frey, R.D., and Kuehl, H.
 TITLE: Method for the specific amplification and detection of DNA and RNA
 METHOD: Method for the specific amplification and detection of DNA and RNA
 JOURNAL: Patent: EP 0766008 A 21 03 MAR 1998;
 COMMENT: BOEHRINGER MANNHEIM GMBH (DE)
 FEATURES: Other publication JP 9079299 970121;
 SOURCE: Location/Qualifiers
 1..26
 /organism "unidentified"
 /db_xref "taxon:32644"

Query Match 52.4%; Score 22; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

21 TGAAGGTGGAGTCAAGGATT 42
 |||||||
 1 TGAAGGTGGAGTCAAGGATT 22

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||||||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 6
 AR028444 AR028444 26 bp RNA linear PAT 29-SEP-1999
 LOCUS Sequence 26 bp
 DEFINITION AR028444
 ACCESSION AR028444
 VERSION AR028444.1 GI:5949417
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 26)
 PRICE, D.K. and Teiland, C.M.
 TITLE Method for detecting prostate cells
 JOURNAL Patent: US 585673-A 5 12 JAN-1999;
 FEATURES location/Qualifiers
 source 1..26 /organism="unknown"

BASE COUNT 6 a 3 c 10 g 7 t

ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||||||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 7
 AR075383 AR075383 26 bp DNA linear PAT 30-AUG-2000
 LOCUS Sequence 26 bp
 DEFINITION AR075383
 ACCESSION AR075383
 VERSION AR075383.1 GI:10002193
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 26)
 WILLIAMS, S.K. and Stopeck, A.
 TITLE Implants possessing a surface of endothelial cells
 JOURNAL genetically modified to inhibit intimal thickening
 FEATURES Patent: US 597972-A 3 28-SEP-1999;
 location/Qualifiers
 source 1..26 /organism="unknown"

BASE COUNT 6 a 3 c 10 g 7 t

ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||||||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 8
 AX015219 AX015219 26 bp DNA linear PAT 07-SEP-2000
 LOCUS Sequence 26 bp
 DEFINITION AX015219
 ACCESSION AX015219
 VERSION AX015219.1 GI:10041252
 KEYWORDS
 SOURCE

SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Antel, J.P. and Prat, A.
 TITLE Bradykinin receptor as marker for inflammatory diseases
 JOURNAL Patent: WO 9951987-A 1 14-OCT-1999;
 FEATURES location/Qualifiers
 source 1..26 /organism="synthetic construct"
 /label="luciferase"
 /note="GAPDH 5' primer"

BASE COUNT 6 a 3 c 10 g 7 t

ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||||||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 9
 AX030701 AX030701 26 bp DNA linear PAT 20-SEP-2000
 LOCUS Sequence 26 bp
 DEFINITION AX030701
 ACCESSION AX030701
 VERSION AX030701.1 GI:10278222
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 26)
 Kuebler, H. and Frey, B.D.
 TITLE Method for the specific amplification and detection of dna and rna
 JOURNAL Patent: EP 0745687-A 21 04-DEC-1996;
 FEATURES location/Qualifiers
 source 1..26 /organism="unidentified"
 /label="luciferase"

BASE COUNT 6 a 3 c 10 g 7 t

ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||||||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 10
 AX166503 AX166503 26 bp DNA linear PAT 25-JUN-2001
 LOCUS Sequence 26 bp
 DEFINITION AX166503
 ACCESSION AX166503
 VERSION AX166503.1 GI:14546851
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 26)
 HOLLIGER, D., Muller, J.J., van, X., Miao, R.K., Bailey, D.A. and
 TITLE Methods and compositions relating to bacteriophage/pericapsid
 JOURNAL increasing factor like polypeptides and polynucleotides
 PATENT: WO 0136478 A 158 25-MAY 2001;
 INSECO, INC. (US)

FEATURES

SOURCE

1..26
/organism="Synthetic Construct"
/db="taxon:32630"
/note="Chemically Synthesized"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.033;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TGAAGTGGAGTCAACGGATT 42
|||||

DB 1 TGAAGTGGAGTCAACGGATT 22

RESULT 11

AX174821

LOCUS

DEFINITION

SEQUENCE 49 FROM PATENT WO0144282.

VERSION

AX174821.1 01-14-98017

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 26)

AUTHORS

White, J. A., and Gosh, K. A.

TITLE

Polypeptides, encoding nucleic acids and methods of use

JOURNAL

Patent: WO 0144282-A 49 21-JUN-2001;

The Burroughs Institute (US)

FEATURES

SOURCE

1..26

/organism="Synthetic Construct"

/db="taxon:32630"

/note="Synthetic primer"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.033;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TGAAGTGGAGTCAACGGATT 42
|||||

DB 1 TGAAGTGGAGTCAACGGATT 22

RESULT 12

AX175502

LOCUS

DEFINITION

SEQUENCE 41 FROM PATENT WO0144443.

VERSION

AX175502.1 01-14-98045

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 26)

AUTHORS

White, J. A., and Gosh, K. A.

TITLE

Polypeptides, encoding nucleic acids and methods of use

JOURNAL

Patent: WO 0144443-A 41 21-JUN-2001;

The Burroughs Institute (US)

FEATURES

SOURCE

1..26

/organism="Human sapiens"

/db="taxon:9606"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.033;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Prod. No. 0.033;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TGAAGTGGAGTCAACGGATT 42
|||||

DB 1 TGAAGTGGAGTCAACGGATT 22

RESULT 13
AX175510
LOCUS
DEFINITION
SEQUENCE 49 FROM PATENT WO0144443.

VERSION
AX175510
AX175510.1 01-14-98053

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 26)

AUTHORS

White, J. A., and Gosh, K. A.

TITLE

Polypeptides, encoding nucleic acids and methods of use

JOURNAL

Patent: WO 0144443-A 49 21-JUN-2001;

The Burroughs Institute (US)

FEATURES

SOURCE

1..26

/organism="Human sapiens"

/db="taxon:9606"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.033;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TGAAGTGGAGTCAACGGATT 42
|||||

DB 1 TGAAGTGGAGTCAACGGATT 22

RESULT 14

AX298289

LOCUS

DEFINITION

SEQUENCE 5 FROM PATENT WO0184768.

VERSION

AX298289.1 01-12-98006

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 26)

AUTHORS

White, J. A., and Gosh, K. A.

TITLE

Polypeptides, encoding nucleic acids and methods of use

JOURNAL

Patent: WO 0184768-A 5 08 NOV 2001;

The Burroughs Institute (US)

FEATURES

SOURCE

1..26

/organism="Synthetic Construct"

/db="taxon:32630"

/note="Primer 3"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.033;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TGAAGTGGAGTCAACGGATT 42
|||||

DB 1 TGAAGTGGAGTCAACGGATT 22

RESULT 15

AX300719 AX300719 26 bp DNA linear PAT 30 NOV 2001
 LOCUS Sequence 5 from Patent WO0185954.
 DEFINITION AX300719
 ACCESSION AX300719
 VERSION AX300719.1 GI:17382022
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 1 artificial sequences.
 REFERENCE
 1 Schart, R. and Doecker, K.
 TITLE Serine-threonine Kinase-3
 JOURNAL Patent: WO 0185954-A 5 15-NOV-2001.
 MERCK PATENT GmbH (DE)
 FEATURES
 source location/qualifiers
 1..26
 /organism="synthetic construct"
 /db_xref="taxon:22630"
 /note="Primer 4"
 BASE COUNT 6 a 3 c 10 g 7 t
 ORIGIN
 Query Match 52.1%, Score 22, DB 6, Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 21 TCAAGCTGGAGTCACGGGATT 42
 ID 1 TCAAGCTGGAGTCACGGGATT 22

Search completed: April 17, 2003, 20:40:56
 Job time : 23049 secs

PT Novel G protein-coupled receptor, HSPRBM7 polypeptide, useful for
PT treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative
PT colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,
PT osteoarthritis

XX Example 4: Page 77; 146pp; English

PS The present invention relates to the isolation of a novel human
CC G-protein coupled receptor (GPCR) (HSPRBM7), and the polynucleotide
CC sequence encoding it. The HSPRBM7 polypeptide and polynucleotide
CC are useful for preventing, treating or ameliorating a disease,
CC disorder or condition related to the colon, brain, ovaries, thymus,
CC lungs or immune system. They are particularly useful for the
CC treatment or prevention of cancers, immune disorders, neurological
CC disorders, and diseases related to the brain, ovaries, thymus or
CC lungs. The polynucleotide sequence is useful for diagnosing or
CC determining susceptibility to infections such as bacterial, fungal,
CC protozoan and viral infections, particularly infection caused by
CC human immunodeficiency virus (HIV or HTV 2). The present sequence
CC represents a probe used for DNA encoding human GPCR
CC (D-glyceraldehyde-3-phosphate dehydrogenase) in the examples of the
CC present invention.

CC Sequence 28 BP; 6 A; 11 G; 3 G; 8 T; 0 other:

Query Match 57.1%; Score 24; DB 24; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00026; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 GGTGAAGTGGAGTCAACGATT 42

26 GGTGAAGTGGAGTCAACGATT 3

RESULT 4

ABR4820/C

ABR4820 standard; DNA: 26 BP.

AC ABR4820;

XX 13-AUG-2002 (first entry)

DE Human glyceraldehyde phosphate dehydrogenase PCR probe.

XX Human PCR; ss: G protein coupled receptor, HSPRBM7; spinal chord;

KM spinal chord-related disorder, breast cancer, neoplastic disease;

KM brain disorder, leukemic myeloma; immunological disorder; probe;

KM cholelithiasis, Grave's disease, osteoarthritis, asthma,

KM neurological disorder, dementia, depression, Alzheimer's disease,

KM Down's syndrome, epilepsy; intracellular calcium level; NFAT;

KM nuclear factor activation of transcription element.

XX Homo sapiens.

OS Homo sapiens.

XX WC200226987-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001WO-US30351.

XX 27-SEP-2000; 2000US-235731P.

XX 14-FEB-2001; 2001US-268280P.

XX 28-AUG-2001; 2001US-315423P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Battaglini P., Feder JN., Minter G., Ramakrishnan CS., Westphal F.,

XX Harker RP., Caruso A., Barber L., Kornacker MG.

XX WP1: 2002-435195/46.

XX Novel human G protein coupled receptor BMT7 (HSPRBM7) polypeptide,

XX useful for modulators of HSPRBM7 activity that are useful for treating

PT leukemia, cholelithiasis, Graves' disease, epilepsy, dementia,

PT depression

XX Example 4; Page 77; 170pp; English.

PS The invention relates to an isolated polypeptide (1) comprising amino

CC acid sequence that is at least 90% identical to a polypeptide fragment of

CC a fully defined human G protein-coupled receptor BMT7 (HSPRBM7)

CC polypeptide, or variant, allelic variant or species homologue.

CC Also included are polynucleotides encoding the above polypeptides,

CC expression vectors, host cells, and HSPRBM7 antibodies and modulators

CC of HSPRBM7. HSPRBM7 and its polynucleotide are useful for diagnosis

CC prevention, treating or ameliorating a medical condition, e.g. a disease,

CC disorder, or a condition related to brain, breast, gastrointestinal or

CC muscular/skeletal systems, such that thalamus, corpus callosum,

CC cerebellum, caudate nucleus, amygdala, substantia nigra,

CC hippocampus, brain, breast, colon, and disorders related to spinal

CC breast cancer, neoplastic diseases, and disorders related to spinal

CC chord and brain. An antagonist or inhibitor of (1) identified using (1)

CC is useful for treating a neoplastic disorder such as leukemia, myeloma,

CC immunological disorders such as cholelithiasis, Graves' disease,

CC osteoarthritis, asthma, neurological disorders such as dementia,

CC depression, Alzheimer's disease, Down's syndrome and epilepsy.

CC HSPRBM7, its polynucleotide and agonists or antagonists of the

CC polypeptide are useful for modulating intracellular calcium levels,

CC modulating cytoskeletal signaling pathways and modulating nuclear

CC factor activation of transcription (NFAT) element associated signalling

CC pathways. The present sequence is a PCR probe used in an experiment to

CC quantify HSPRBM7 mRNA.

XX Sequence 28 BP; 6 A; 11 G; 3 G; 8 T; 0 other:

Query Match 57.1%; Score 24; DB 24; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00026;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 GGTGAAGTGGAGTCAACGATT 42

26 GGTGAAGTGGAGTCAACGATT 3

RESULT 5

ABR70642/C

ABR70642 standard; DNA: 28 BP.

AC ABR70642;

XX 16-MAY-2002 (first entry)

DE GAPDH probe.

XX Human; G-protein coupled receptor; HSPRBM7; small intestine; colon;

XX testis; cancer; PCR; primer; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WC200226987-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001WO-US30614.

XX 27-SEP-2000; 2000US-236602P.

XX 19-JUL-2001; 2001US-406604P.

XX 28-AUG-2001; 2001US-315412P.

XX (PRIM) PRISTOL-MYERS SQUIBB CO.

XX Feder JN., Minter G., Ramakrishnan CS., Hawken JR., Caruso A., Barber L.,

XX Kornacker MG.

XX WP1: 2002-202774/41.

XX Novel human G protein coupled receptor BMT7 (HSPRBM7) polypeptide,

XX useful for modulators of HSPRBM7 activity that are useful for treating

11 Novel isolated polypeptide encoding a human G protein coupled
 12 receptor, both useful for treating condition of the small intestine,
 13 colon, or testis -
 14
 15 Example 4: Page 75; 174pp; English.
 16
 17 The invention relates to an isolated polypeptide encoding a human G-
 18 protein coupled receptor, hGPRH46. The polypeptide and polynucleotide
 19 are used to treat and diagnose a disease, disorder or condition
 20 associated with the small intestine, colon, or testis, particularly
 21 cancer. AAK70640-AAK70648 represent human G-protein coupled receptor
 22 coding sequences and PCR primers of the invention.
 23
 24 Sequence 28 BP: 6 A; 11 C; 4 G; 8 T; 0 other;
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525
 526
 527
 528
 529
 530
 531
 532
 533
 534
 535
 536
 537
 538
 539
 540
 541
 542
 543
 544
 545
 546
 547
 548
 549
 550
 551
 552
 553
 554
 555
 556
 557
 558
 559
 560
 561
 562
 563
 564
 565
 566
 567
 568
 569
 570
 571
 572
 573
 574
 575
 576
 577
 578
 579
 580
 581
 582
 583
 584
 585
 586
 587
 588
 589
 590
 591
 592
 593
 594
 595
 596
 597
 598
 599
 600
 601
 602
 603
 604
 605
 606
 607
 608
 609
 610
 611
 612
 613
 614
 615
 616
 617
 618
 619
 620
 621
 622
 623
 624
 625
 626
 627
 628
 629
 630
 631
 632
 633
 634
 635
 636
 637
 638
 639
 640
 641
 642
 643
 644
 645
 646
 647
 648
 649
 650
 651
 652
 653
 654
 655
 656
 657
 658
 659
 660
 661
 662
 663
 664
 665
 666
 667
 668
 669
 670
 671
 672
 673
 674
 675
 676
 677
 678
 679
 680
 681
 682
 683
 684
 685
 686
 687
 688
 689
 690
 691
 692
 693
 694
 695
 696
 697
 698
 699
 700
 701
 702
 703
 704
 705
 706
 707
 708
 709
 710
 711
 712
 713
 714
 715
 716
 717
 718
 719
 720
 721
 722
 723
 724
 725
 726
 727
 728
 729
 730
 731
 732
 733
 734
 735
 736
 737
 738
 739
 740
 741
 742
 743
 744
 745
 746
 747
 748
 749
 750
 751
 752
 753
 754
 755
 756
 757
 758
 759
 760
 761
 762
 763
 764
 765
 766
 767
 768
 769
 770
 771
 772
 773
 774
 775
 776
 777
 778
 779
 780
 781
 782
 783
 784
 785
 786
 787
 788
 789
 790
 791
 792
 793
 794
 795
 796
 797
 798
 799
 800
 801
 802
 803
 804
 805
 806
 807
 808
 809
 810
 811
 812
 813
 814
 815
 816
 817
 818
 819
 820
 821
 822
 823
 824
 825
 826
 827
 828
 829
 830
 831
 832
 833
 834
 835
 836
 837
 838
 839
 840
 841
 842
 843
 844
 845
 846
 847
 848
 849
 850
 851
 852
 853
 854
 855
 856
 857
 858
 859
 860
 861
 862
 863
 864
 865
 866
 867
 868
 869
 870
 871
 872
 873
 874
 875
 876
 877
 878
 879
 880
 881
 882
 883
 884
 885
 886
 887
 888
 889
 890
 891
 892
 893
 894
 895
 896
 897
 898
 899
 900
 901
 902
 903
 904
 905
 906
 907
 908
 909
 910
 911
 912
 913
 914
 915
 916
 917
 918
 919
 920
 921
 922
 923
 924
 925
 926
 927
 928
 929
 930
 931
 932
 933
 934
 935
 936
 937
 938
 939
 940
 941
 942
 943
 944
 945
 946
 947
 948
 949
 950
 951
 952
 953
 954
 955
 956
 957
 958
 959
 960
 961
 962
 963
 964
 965
 966
 967
 968
 969
 970
 971
 972
 973
 974
 975
 976
 977
 978
 979
 980
 981
 982
 983
 984
 985
 986
 987
 988
 989
 990
 991
 992
 993
 994
 995
 996
 997
 998
 999
 1000

1001
 1002
 1003
 1004
 1005
 1006
 1007
 1008
 1009
 1010
 1011
 1012
 1013
 1014
 1015
 1016
 1017
 1018
 1019
 1020
 1021
 1022
 1023
 1024
 1025
 1026
 1027
 1028
 1029
 1030
 1031
 1032
 1033
 1034
 1035
 1036
 1037
 1038
 1039
 1040
 1041
 1042
 1043
 1044
 1045
 1046
 1047
 1048
 1049
 1050
 1051
 1052
 1053
 1054
 1055
 1056
 1057
 1058
 1059
 1060
 1061
 1062
 1063
 1064
 1065
 1066
 1067
 1068
 1069
 1070
 1071
 1072
 1073
 1074
 1075
 1076
 1077
 1078
 1079
 1080
 1081
 1082
 1083
 1084
 1085
 1086
 1087
 1088
 1089
 1090
 1091
 1092
 1093
 1094
 1095
 1096
 1097
 1098
 1099
 1100
 1101
 1102
 1103
 1104
 1105
 1106
 1107
 1108
 1109
 1110
 1111
 1112
 1113
 1114
 1115
 1116
 1117
 1118
 1119
 1120
 1121
 1122
 1123
 1124
 1125
 1126
 1127
 1128
 1129
 1130
 1131
 1132
 1133
 1134
 1135
 1136
 1137
 1138
 1139
 1140
 1141
 1142
 1143
 1144
 1145
 1146
 1147
 1148
 1149
 1150
 1151
 1152
 1153
 1154
 1155
 1156
 1157
 1158
 1159
 1160
 1161
 1162
 1163
 1164
 1165
 1166
 1167
 1168
 1169
 1170
 1171
 1172
 1173
 1174
 1175
 1176
 1177
 1178
 1179
 1180
 1181
 1182
 1183
 1184
 1185
 1186
 1187
 1188
 1189
 1190
 1191
 1192
 1193
 1194
 1195
 1196
 1197
 1198
 1199
 1200
 1201
 1202
 1203
 1204
 1205
 1206
 1207
 1208
 1209
 1210
 1211
 1212
 1213
 1214
 1215
 1216
 1217
 1218
 1219
 1220
 1221
 1222
 1223
 1224
 1225
 1226
 1227
 1228
 1229
 1230
 1231
 1232
 1233
 1234
 1235
 1236
 1237
 1238
 1239
 1240
 1241
 1242
 1243
 1244
 1245
 1246
 1247
 1248
 1249
 1250
 1251
 1252
 1253
 1254
 1255
 1256
 1257
 1258
 1259
 1260
 1261
 1262
 1263
 1264
 1265
 1266
 1267
 1268
 1269
 1270
 1271
 1272
 1273
 1274
 1275
 1276
 1277
 1278
 1279
 1280
 1281
 1282
 1283
 1284
 1285
 1286
 1287
 1288
 1289
 1290
 1291
 1292
 1293
 1294
 1295
 1296
 1297
 1298
 1299
 1300
 1301
 1302
 1303
 1304
 1305
 1306
 1307
 1308
 1309
 1310
 1311
 1312
 1313
 1314
 1315
 1316
 1317
 1318
 1319
 1320
 1321
 1322
 1323
 1324
 1325
 1326
 1327
 1328
 1329
 1330
 1331
 1332
 1333
 1334
 1335
 1336
 1337
 1338
 1339
 1340
 1341
 1342
 1343
 1344
 1345
 1346
 1347
 1348
 1349
 1350
 1351
 1352
 1353
 1354
 1355
 1356
 1357
 1358
 1359
 1360
 1361
 1362
 1363
 1364
 1365
 1366
 1367
 1368
 1369
 1370
 1371
 1372
 1373
 1374
 1375
 1376
 1377
 1378
 1379
 1380
 1381
 1382
 1383
 1384
 1385
 1386
 1387
 1388
 1389
 1390
 1391
 1392
 1393
 1394
 1395
 1396
 1397
 1398
 1399
 1400
 1401
 1402
 1403
 1404
 1405
 1406
 1407
 1408
 1409
 1410
 1411
 1412
 1413
 1414
 1415
 1416
 1417
 1418
 1419
 1420
 1421
 1422
 1423
 1424
 1425
 1426
 1427
 1428
 1429
 1430
 1431
 1432
 1433
 1434
 1435
 1436
 1437
 1438
 1439
 1440
 1441
 1442
 1443
 1444
 1445
 1446
 1447
 1448
 1449
 1450
 1451
 1452
 1453
 1454
 1455
 1456
 1457
 1458
 1459
 1460
 1461
 1462
 1463
 1464
 1465
 1

OY 21 TGAAGCTGGAGTCAACGGATT 42
 |||
 DB 1 TGAAGCTGGAGTCAACGGATT 22

RESULT 8
 AAT29240
 ID AAT29240 standard; DNA; 26 BP.

AC AAT29240:
 XX 16-JUL-1996 (first entry)

DE Glyceraldehyde-3-phosphate-dehydrogenase sense primer.

XX 31-DEC-1993 The stable dehydrogenase interlockin-8;
 KM sense primer; antisense primer; polymerase chain reaction; PCR;
 KM CagB; CagC; antigen infection; peptic ulcer; gastric carcinoma;
 KM antisense oligonucleotide; treatment; prevention; diagnosis;
 KM attenuation; vaccine; ss

XX Synthetic.

OS K09612925-A1

PN 02-MAY-1996.

PD 20-OCT-1995; 9450-0014659

PR 21-OCT-1994; 9405-0327494.

XX (YVVA-) HIV VANDPRIT

FA Blaser MJ, Sharma SA, Tummuru MKR;

XX WPI: 1995-23653/22.

XX DNA encoding Helicobacter pylori CagB and CagC antigens;
 PT F-PCR; PCR; assay for diagnosis of pylori infection and to
 PT indicate predilection to peptic ulceration or gastric cancer

XX Example 3: Page 44; 74pp; English.

XX In a study aimed to show that the H. pylori CagB/C gene (see
 CC AAT14373) is required for interleukin-8 (IL-8) induction in gastric
 CC cells, confluent monolayer cultures of the human gastric carcinoma
 CC cell line AGS (ATCC CRL 1739) were incubated with live H. pylori
 CC at a bacterium:cell ratio of 1000:1. Total RNA was extracted from
 CC the cultured cells and used to synthesize cDNA, which was used in
 CC a PCR reaction with primers for human IL-8 (see AAT29242 and AAT29243)
 CC and primers for human glyceraldehyde-3-phosphate-dehydrogenase as
 CC control primers, i.e., this sense primer and the antisense primer
 CC AAT29241. Detection of the CagB or CagC proteins using antibodies,
 CC or detection of the DNA using specific probes or primers can be
 CC used to diagnose H. pylori infection and to indicate predilection
 CC to peptic ulcers or gastric carcinoma. Antisense oligonucleotides
 CC to regulatory regions of the DNA can be used in therapy. Mutant
 CC H. pylori deficient in CagB (ATCC 55611) or CagC (ATCC 55612) are
 CC attenuated because they do not stimulate synthesis of IL-8 in
 CC epithelial cells.

XX Sequence 26 BP; 6 A; 3 C; 10 G; 7 T; 0 other;

XX Query Match 52.4%; Score 22; DB 17; Length 26;

XX Best Local Similarity 100.0%; Pred. No. 0.0037;

OY 21 TGAAGCTGGAGTCAACGGATT 42
 |||
 DB 1 TGAAGCTGGAGTCAACGGATT 22

RESULT 9

AAT70484
 ID AAT70484 standard; DNA; 26 BP
 XX
 AC AAT70484:

DE 28-AUG-1997 (first entry)

DE Dystrophin forward primer.

XX primer; PCR; polymerase chain reaction; enzyme mixture; polymerase;
 KM proof-reading activity; Pfu. Two Thermus aquaticus wossl;
 KM thermostable; AMV; reverse transcriptase; Moloney; amplification;
 KM Avian myeloblastosis virus; oncogeny; murine leukemia virus; ss.

XX Synthetic.

OS EP45087-A1.

PN 04-DEC-1996.

PD 09-APR-1996; 90EP 0105571.

PR 08-APR-1995; 95EP-0105346.

XX (Boehr) BOEHRINGER MANNHEIM GMBH.

PN Frey B, Kuebler H;

XX WPI: 1997 013703/22.

XX Specific amplification of short nucleic acid fragments - using two

XX thermophilic polymerase(s) one with, the other without,

XX proof reading activity, to improve yield and specificity

XX Example 7; Page 5; 31pp; German.

XX A novel method for the specific amplification of short, single- or
 CC double-stranded nucleic acid fragments can be carried out in presence of
 CC at least one primer pair, pH 7-9.5 buffer, all dNTP required for DNA
 CC extension and a mixture of two thermophilic polymerases, one
 CC with proofreading activity (e.g., two polymerase from Thermococcus woessli)
 CC and the other (e.g., tag polymerase from Thermus aquaticus) without such
 CC activity. After optimal separation of double stranded molecules, the
 CC extension reaction is carried out at at least 70deg C for 5 seconds to 8
 CC minutes. The method is used to amplify DNA fragments up to 3 kb long,
 CC esp. for detection of these fragments in samples of biological fluid.
 CC The enzyme mixt. can also be used to label DNA fragments with modified
 CC nucleotides. The process provides increased yields and specificity in
 CC amplification of short nucleic acid fragments. The enzyme mixture can be
 CC used with reverse transcriptase in an RT-PCR reaction. AAT70482-85 are
 CC primers used in an assay to show the reaction conditions for use of
 CC the AMV-RT and the two/tag enzyme mixture. A 1851 bp fragment of the
 CC Dystrophin cDNA was amplified using AAT70484-85.

XX Sequence 26 BP; 6 A; 3 C; 10 G; 7 T; 0 other;

XX Query Match 52.4%; Score 22; DB 18; Length 26;

XX Best Local Similarity 100.0%; Pred. No. 0.0037;

OY 21 TGAAGCTGGAGTCAACGGATT 42
 |||
 DB 1 TGAAGCTGGAGTCAACGGATT 22

XX PRSOUT 10
 AAV46348

XX ID AAV46348 standard; DNA; 26 BP.

XX AC AAV46348;

XX DT 11-NOV-1998 (first entry)

CC activity and screening for agents that treat inflammatory diseases. The
 CC diseases can be multiple sclerosis, rheumatoid arthritis,
 CC osteoarthritis, Crohn's disease, ulcerative colitis or lupus.
 CC erythema multiforme, which can be more expensive and time-consuming. Sequences
 CC AA23113-114 represent G3PDH primers.
 CC XX

Sequence 26 BP: 6 A; 3 G; 10 G; 7 T; 0 other.

Query Match 52.48, Score 22, DP 20, Length 26
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TGAAGTCGAGTCACGAGATT 42
 ID 1 TGAAGTCGAGTCACGAGATT 22

RESULT 13
 AA21557
 ID AA21557 standard; DNA: 26 BP.
 XX
 AC AA21557;
 XX
 DE 01-DEC-1999 (first entry)
 XX
 DE 5' PCR primer used for amplification of G3PDH gene.
 XX
 KM G3PDH: gamma interferon; smooth muscle cell proliferation;
 KM intimal thickening; thrombosis; vascular graft; endothelial cell; valve;
 KM genetically modified; endovascular graft; artificial blood vessel;
 KM arteriosclerosis; medial arteriosclerosis; heart failure; heart failure;
 KM arterial aneurysm; organ failure; ischemia; blood clot; thrombin; ss;
 KM g1/gc311-lyb-3-phosphate-4-hydroxy-2-oxo-3-oxo-4-oxo-5-oxo-6-oxo-7-oxo-8-oxo-9-oxo-10-oxo-11-oxo-12-oxo-13-oxo-14-oxo-15-oxo-16-oxo-17-oxo-18-oxo-19-oxo-20-oxo-21-oxo-22-oxo-23-oxo-24-oxo-25-oxo-26-oxo-27-oxo-28-oxo-29-oxo-30-oxo-31-oxo-32-oxo-33-oxo-34-oxo-35-oxo-36-oxo-37-oxo-38-oxo-39-oxo-40-oxo-41-oxo-42-oxo-43-oxo-44-oxo-45-oxo-46-oxo-47-oxo-48-oxo-49-oxo-50-oxo-51-oxo-52-oxo-53-oxo-54-oxo-55-oxo-56-oxo-57-oxo-58-oxo-59-oxo-60-oxo-61-oxo-62-oxo-63-oxo-64-oxo-65-oxo-66-oxo-67-oxo-68-oxo-69-oxo-70-oxo-71-oxo-72-oxo-73-oxo-74-oxo-75-oxo-76-oxo-77-oxo-78-oxo-79-oxo-80-oxo-81-oxo-82-oxo-83-oxo-84-oxo-85-oxo-86-oxo-87-oxo-88-oxo-89-oxo-90-oxo-91-oxo-92-oxo-93-oxo-94-oxo-95-oxo-96-oxo-97-oxo-98-oxo-99-oxo-100-oxo-101-oxo-102-oxo-103-oxo-104-oxo-105-oxo-106-oxo-107-oxo-108-oxo-109-oxo-110-oxo-111-oxo-112-oxo-113-oxo-114-oxo-115-oxo-116-oxo-117-oxo-118-oxo-119-oxo-120-oxo-121-oxo-122-oxo-123-oxo-124-oxo-125-oxo-126-oxo-127-oxo-128-oxo-129-oxo-130-oxo-131-oxo-132-oxo-133-oxo-134-oxo-135-oxo-136-oxo-137-oxo-138-oxo-139-oxo-140-oxo-141-oxo-142-oxo-143-oxo-144-oxo-145-oxo-146-oxo-147-oxo-148-oxo-149-oxo-150-oxo-151-oxo-152-oxo-153-oxo-154-oxo-155-oxo-156-oxo-157-oxo-158-oxo-159-oxo-160-oxo-161-oxo-162-oxo-163-oxo-164-oxo-165-oxo-166-oxo-167-oxo-168-oxo-169-oxo-170-oxo-171-oxo-172-oxo-173-oxo-174-oxo-175-oxo-176-oxo-177-oxo-178-oxo-179-oxo-180-oxo-181-oxo-182-oxo-183-oxo-184-oxo-185-oxo-186-oxo-187-oxo-188-oxo-189-oxo-190-oxo-191-oxo-192-oxo-193-oxo-194-oxo-195-oxo-196-oxo-197-oxo-198-oxo-199-oxo-200-oxo-201-oxo-202-oxo-203-oxo-204-oxo-205-oxo-206-oxo-207-oxo-208-oxo-209-oxo-210-oxo-211-oxo-212-oxo-213-oxo-214-oxo-215-oxo-216-oxo-217-oxo-218-oxo-219-oxo-220-oxo-221-oxo-222-oxo-223-oxo-224-oxo-225-oxo-226-oxo-227-oxo-228-oxo-229-oxo-230-oxo-231-oxo-232-oxo-233-oxo-234-oxo-235-oxo-236-oxo-237-oxo-238-oxo-239-oxo-240-oxo-241-oxo-242-oxo-243-oxo-244-oxo-245-oxo-246-oxo-247-oxo-248-oxo-249-oxo-250-oxo-251-oxo-252-oxo-253-oxo-254-oxo-255-oxo-256-oxo-257-oxo-258-oxo-259-oxo-260-oxo-261-oxo-262-oxo-263-oxo-264-oxo-265-oxo-266-oxo-267-oxo-268-oxo-269-oxo-270-oxo-271-oxo-272-oxo-273-oxo-274-oxo-275-oxo-276-oxo-277-oxo-278-oxo-279-oxo-280-oxo-281-oxo-282-oxo-283-oxo-284-oxo-285-oxo-286-oxo-287-oxo-288-oxo-289-oxo-290-oxo-291-oxo-292-oxo-293-oxo-294-oxo-295-oxo-296-oxo-297-oxo-298-oxo-299-oxo-300-oxo-301-oxo-302-oxo-303-oxo-304-oxo-305-oxo-306-oxo-307-oxo-308-oxo-309-oxo-310-oxo-311-oxo-312-oxo-313-oxo-314-oxo-315-oxo-316-oxo-317-oxo-318-oxo-319-oxo-320-oxo-321-oxo-322-oxo-323-oxo-324-oxo-325-oxo-326-oxo-327-oxo-328-oxo-329-oxo-330-oxo-331-oxo-332-oxo-333-oxo-334-oxo-335-oxo-336-oxo-337-oxo-338-oxo-339-oxo-340-oxo-341-oxo-342-oxo-343-oxo-344-oxo-345-oxo-346-oxo-347-oxo-348-oxo-349-oxo-350-oxo-351-oxo-352-oxo-353-oxo-354-oxo-355-oxo-356-oxo-357-oxo-358-oxo-359-oxo-360-oxo-361-oxo-362-oxo-363-oxo-364-oxo-365-oxo-366-oxo-367-oxo-368-oxo-369-oxo-370-oxo-371-oxo-372-oxo-373-oxo-374-oxo-375-oxo-376-oxo-377-oxo-378-oxo-379-oxo-380-oxo-381-oxo-382-oxo-383-oxo-384-oxo-385-oxo-386-oxo-387-oxo-388-oxo-389-oxo-390-oxo-391-oxo-392-oxo-393-oxo-394-oxo-395-oxo-396-oxo-397-oxo-398-oxo-399-oxo-400-oxo-401-oxo-402-oxo-403-oxo-404-oxo-405-oxo-406-oxo-407-oxo-408-oxo-409-oxo-410-oxo-411-oxo-412-oxo-413-oxo-414-oxo-415-oxo-416-oxo-417-oxo-418-oxo-419-oxo-420-oxo-421-oxo-422-oxo-423-oxo-424-oxo-425-oxo-426-oxo-427-oxo-428-oxo-429-oxo-430-oxo-431-oxo-432-oxo-433-oxo-434-oxo-435-oxo-436-oxo-437-oxo-438-oxo-439-oxo-440-oxo-441-oxo-442-oxo-443-oxo-444-oxo-445-oxo-446-oxo-447-oxo-448-oxo-449-oxo-450-oxo-451-oxo-452-oxo-453-oxo-454-oxo-455-oxo-456-oxo-457-oxo-458-oxo-459-oxo-460-oxo-461-oxo-462-oxo-463-oxo-464-oxo-465-oxo-466-oxo-467-oxo-468-oxo-469-oxo-470-oxo-471-oxo-472-oxo-473-oxo-474-oxo-475-oxo-476-oxo-477-oxo-478-oxo-479-oxo-480-oxo-481-oxo-482-oxo-483-oxo-484-oxo-485-oxo-486-oxo-487-oxo-488-oxo-489-oxo-490-oxo-491-oxo-492-oxo-493-oxo-494-oxo-495-oxo-496-oxo-497-oxo-498-oxo-499-oxo-500-oxo-501-oxo-502-oxo-503-oxo-504-oxo-505-oxo-506-oxo-507-oxo-508-oxo-509-oxo-510-oxo-511-oxo-512-oxo-513-oxo-514-oxo-515-oxo-516-oxo-517-oxo-518-oxo-519-oxo-520-oxo-521-oxo-522-oxo-523-oxo-524-oxo-525-oxo-526-oxo-527-oxo-528-oxo-529-oxo-530-oxo-531-oxo-532-oxo-533-oxo-534-oxo-535-oxo-536-oxo-537-oxo-538-oxo-539-oxo-540-oxo-541-oxo-542-oxo-543-oxo-544-oxo-545-oxo-546-oxo-547-oxo-548-oxo-549-oxo-550-oxo-551-oxo-552-oxo-553-oxo-554-oxo-555-oxo-556-oxo-557-oxo-558-oxo-559-oxo-560-oxo-561-oxo-562-oxo-563-oxo-564-oxo-565-oxo-566-oxo-567-oxo-568-oxo-569-oxo-570-oxo-571-oxo-572-oxo-573-oxo-574-oxo-575-oxo-576-oxo-577-oxo-578-oxo-579-oxo-580-oxo-581-oxo-582-oxo-583-oxo-584-oxo-585-oxo-586-oxo-587-oxo-588-oxo-589-oxo-590-oxo-591-oxo-592-oxo-593-oxo-594-oxo-595-oxo-596-oxo-597-oxo-598-oxo-599-oxo-600-oxo-601-oxo-602-oxo-603-oxo-604-oxo-605-oxo-606-oxo-607-oxo-608-oxo-609-oxo-610-oxo-611-oxo-612-oxo-613-oxo-614-oxo-615-oxo-616-oxo-617-oxo-618-oxo-619-oxo-620-oxo-621-oxo-622-oxo-623-oxo-624-oxo-625-oxo-626-oxo-627-oxo-628-oxo-629-oxo-630-oxo-631-oxo-632-oxo-633-oxo-634-oxo-635-oxo-636-oxo-637-oxo-638-oxo-639-oxo-640-oxo-641-oxo-642-oxo-643-oxo-644-oxo-645-oxo-646-oxo-647-oxo-648-oxo-649-oxo-650-oxo-651-oxo-652-oxo-653-oxo-654-oxo-655-oxo-656-oxo-657-oxo-658-oxo-659-oxo-660-oxo-661-oxo-662-oxo-663-oxo-664-oxo-665-oxo-666-oxo-667-oxo-668-oxo-669-oxo-670-oxo-671-oxo-672-oxo-673-oxo-674-oxo-675-oxo-676-oxo-677-oxo-678-oxo-679-oxo-680-oxo-681-oxo-682-oxo-683-oxo-684-oxo-685-oxo-686-oxo-687-oxo-688-oxo-689-oxo-690-oxo-691-oxo-692-oxo-693-oxo-694-oxo-695-oxo-696-oxo-697-oxo-698-oxo-699-oxo-700-oxo-701-oxo-702-oxo-703-oxo-704-oxo-705-oxo-706-oxo-707-oxo-708-oxo-709-oxo-710-oxo-711-oxo-712-oxo-713-oxo-714-oxo-715-oxo-716-oxo-717-oxo-718-oxo-719-oxo-720-oxo-721-oxo-722-oxo-723-oxo-724-oxo-725-oxo-726-oxo-727-oxo-728-oxo-729-oxo-730-oxo-731-oxo-732-oxo-733-oxo-734-oxo-735-oxo-736-oxo-737-oxo-738-oxo-739-oxo-740-oxo-741-oxo-742-oxo-743-oxo-744-oxo-745-oxo-746-oxo-747-oxo-748-oxo-749-oxo-750-oxo-751-oxo-752-oxo-753-oxo-754-oxo-755-oxo-756-oxo-757-oxo-758-oxo-759-oxo-760-oxo-761-oxo-762-oxo-763-oxo-764-oxo-765-oxo-766-oxo-767-oxo-768-oxo-769-oxo-770-oxo-771-oxo-772-oxo-773-oxo-774-oxo-775-oxo-776-oxo-777-oxo-778-oxo-779-oxo-780-oxo-781-oxo-782-oxo-783-oxo-784-oxo-785-oxo-786-oxo-787-oxo-788-oxo-789-oxo-790-oxo-791-oxo-792-oxo-793-oxo-794-oxo-795-oxo-796-oxo-797-oxo-798-oxo-799-oxo-800-oxo-801-oxo-802-oxo-803-oxo-804-oxo-805-oxo-806-oxo-807-oxo-808-oxo-809-oxo-810-oxo-811-oxo-812-oxo-813-oxo-814-oxo-815-oxo-816-oxo-817-oxo-818-oxo-819-oxo-820-oxo-821-oxo-822-oxo-823-oxo-824-oxo-825-oxo-826-oxo-827-oxo-828-oxo-829-oxo-830-oxo-831-oxo-832-oxo-833-oxo-834-oxo-835-oxo-836-oxo-837-oxo-838-oxo-839-oxo-840-oxo-841-oxo-842-oxo-843-oxo-844-oxo-845-oxo-846-oxo-847-oxo-848-oxo-849-oxo-850-oxo-851-oxo-852-oxo-853-oxo-854-oxo-855-oxo-856-oxo-857-oxo-858-oxo-859-oxo-860-oxo-861-oxo-862-oxo-863-oxo-864-oxo-865-oxo-866-oxo-867-oxo-868-oxo-869-oxo-870-oxo-871-oxo-872-oxo-873-oxo-874-oxo-875-oxo-876-oxo-877-oxo-878-oxo-879-oxo-880-oxo-881-oxo-882-oxo-883-oxo-884-oxo-885-oxo-886-oxo-887-oxo-888-oxo-889-oxo-890-oxo-891-oxo-892-oxo-893-oxo-894-oxo-895-oxo-896-oxo-897-oxo-898-oxo-899-oxo-900-oxo-901-oxo-902-oxo-903-oxo-904-oxo-905-oxo-906-oxo-907-oxo-908-oxo-909-oxo-910-oxo-911-oxo-912-oxo-913-oxo-914-oxo-915-oxo-916-oxo-917-oxo-918-oxo-919-oxo-920-oxo-921-oxo-922-oxo-923-oxo-924-oxo-925-oxo-926-oxo-927-oxo-928-oxo-929-oxo-930-oxo-931-oxo-932-oxo-933-oxo-934-oxo-935-oxo-936-oxo-937-oxo-938-oxo-939-oxo-940-oxo-941-oxo-942-oxo-943-oxo-944-oxo-945-oxo-946-oxo-947-oxo-948-oxo-949-oxo-950-oxo-951-oxo-952-oxo-953-oxo-954-oxo-955-oxo-956-oxo-957-oxo-958-oxo-959-oxo-960-oxo-961-oxo-962-oxo-963-oxo-964-oxo-965-oxo-966-oxo-967-oxo-968-oxo-969-oxo-970-oxo-971-oxo-972-oxo-973-oxo-974-oxo-975-oxo-976-oxo-977-oxo-978-oxo-979-oxo-980-oxo-981-oxo-982-oxo-983-oxo-984-oxo-985-oxo-986-oxo-987-oxo-988-oxo-989-oxo-990-oxo-991-oxo-992-oxo-993-oxo-994-oxo-995-oxo-996-oxo-997-oxo-998-oxo-999-oxo-1000-oxo-1001-oxo-1002-oxo-1003-oxo-1004-oxo-1005-oxo-1006-oxo-1007-oxo-1008-oxo-1009-oxo-1010-oxo-1011-oxo-1012-oxo-1013-oxo-1014-oxo-1015-oxo-1016-oxo-1017-oxo-1018-oxo-1019-oxo-1020-oxo-1021-oxo-1022-oxo-1023-oxo-1024-oxo-1025-oxo-1026-oxo-1027-oxo-1028-oxo-1029-oxo-1030-oxo-1031-oxo-1032-oxo-1033-oxo-1034-oxo-1035-oxo-1036-oxo-1037-oxo-1038-oxo-1039-oxo-1040-oxo-1041-oxo-1042-oxo-1043-oxo-1044-oxo-1045-oxo-1046-oxo-1047-oxo-1048-oxo-1049-oxo-1050-oxo-1051-oxo-1052-oxo-1053-oxo-1054-oxo-1055-oxo-1056-oxo-1057-oxo-1058-oxo-1059-oxo-1060-oxo-1061-oxo-1062-oxo-1063-oxo-1064-oxo-1065-oxo-1066-oxo-1067-oxo-1068-oxo-1069-oxo-1070-oxo-1071-oxo-1072-oxo-1073-oxo-1074-oxo-1075-oxo-1076-oxo-1077-oxo-1078-oxo-1079-oxo-1080-oxo-1081-oxo-1082-oxo-1083-oxo-1084-oxo-1085-oxo-1086-oxo-1087-oxo-1088-oxo-1089-oxo-1090-oxo-1091-oxo-1092-oxo-1093-oxo-1094-oxo-1095-oxo-1096-oxo-1097-oxo-1098-oxo-1099-oxo-1100-oxo-1101-oxo-1102-oxo-1103-oxo-1104-oxo-1105-oxo-1106-oxo-1107-oxo-1108-oxo-1109-oxo-1110-oxo-1111-oxo-1112-oxo-1113-oxo-1114-oxo-1115-oxo-1116-oxo-1117-oxo-1118-oxo-1119-oxo-1120-oxo-1121-oxo-1122-oxo-1123-oxo-1124-oxo-1125-oxo-1126-oxo-1127-oxo-1128-oxo-1129-oxo-1130-oxo-1131-oxo-1132-oxo-1133-oxo-1134-oxo-1135-oxo-1136-oxo-1137-oxo-1138-oxo-1139-oxo-1140-oxo-1141-oxo-1142-oxo-1143-oxo-1144-oxo-1145-oxo-1146-oxo-1147-oxo-1148-oxo-1149-oxo-1150-oxo-1151-oxo-1152-oxo-1153-oxo-1154-oxo-1155-oxo-1156-oxo-1157-oxo-1158-oxo-1159-oxo-1160-oxo-1161-oxo-1162-oxo-1163-oxo-1164-oxo-1165-oxo-1166-oxo-1167-oxo-1168-oxo-1169-oxo-1170-oxo-1171-oxo-1172-oxo-1173-oxo-1174-oxo-1175-oxo-1176-oxo-1177-oxo-1178-oxo-1179-oxo-1180-oxo-1181-oxo-1182-oxo-1183-oxo-1184-oxo-1185-oxo-1186-oxo-1187-oxo-1188-oxo-1189-oxo-1190-oxo-1191-oxo-1192-oxo-1193-oxo-1194-oxo-1195-oxo-1196-oxo-1197-oxo-1198-oxo-1199-oxo-1200-oxo-1201-oxo-1202-oxo-1203-oxo-1204-oxo-1205-oxo-1206-oxo-1207-oxo-1208-oxo-1209-oxo-1210-oxo-1211-oxo-1212-oxo-1213-oxo-1214-oxo-1215-oxo-1216-oxo-1217-oxo-1218-oxo-1219-oxo-1220-oxo-1221-oxo-1222-oxo-1223-oxo-1224-oxo-1225-oxo-1226-oxo-1227-oxo-1228-oxo-1229-oxo-1230-oxo-1231-oxo-1232-oxo-1233-oxo-1234-oxo-1235-oxo-1236-oxo-1237-oxo-1238-oxo-1239-oxo-1240-oxo-1241-oxo-1242-oxo-1243-oxo-1244-oxo-1245-oxo-1246-oxo-1247-oxo-1248-oxo-1249-oxo-1250-oxo-1251-oxo-1252-oxo-1253-oxo-1254-oxo-1255-oxo-1256-oxo-1257-oxo-1258-oxo-1259-oxo-1260-oxo-1261-oxo-1262-oxo-1263-oxo-1264-oxo-1265-oxo-1266-oxo-1267-oxo-1268-oxo-1269-oxo-1270-oxo-1271-oxo-1272-oxo-1273-oxo-1274-oxo-1275-oxo-1276-oxo-1277-oxo-1278-oxo-1279-oxo-1280-oxo-1281-oxo-1282-oxo-1283-oxo-1284-oxo-1285-oxo-1286-oxo-1287-oxo-1288-oxo-1289-oxo-1290-oxo-1291-oxo-1292-oxo-1293-oxo-1294-oxo-1295-oxo-1296-oxo-1297-oxo-1298-oxo-1299-oxo-1300-oxo-1301-oxo-1302-oxo-1303-oxo-1304-oxo-1305-oxo-1306-oxo-1307-oxo-1308-oxo-1309-oxo-1310-oxo-1311-oxo-1312-oxo-1313-oxo-1314-oxo-1315-oxo-1316-oxo-1317-oxo-1318-oxo-1319-oxo-1320-oxo-1321-oxo-1322-oxo-1323-oxo-1324-oxo-1325-oxo-1326-oxo-1327-oxo-1328-oxo-1329-oxo-1330-oxo-1331-oxo-1332-oxo-1333-oxo-1334-oxo-1335-oxo-1336-oxo-1337-oxo-1338-oxo-1339-oxo-1340-oxo-1341-oxo-1342-oxo-1343-oxo-1344-oxo-1345-oxo-1346-oxo-1347-oxo-1348-oxo-1349-oxo-1350-oxo-1351-oxo-1352-oxo-1353-oxo-1354-oxo-1355-oxo-1356-oxo-1357-oxo-1358-oxo-1359-oxo-1360-oxo-1361-oxo-1362-oxo-1363-oxo-1364-oxo-1365-oxo-1366-oxo-1367-oxo-1368-oxo-1369-oxo-1370-oxo-1371-oxo-1372-oxo-1373-oxo-1374-oxo-1375-oxo-1376-oxo-1377-oxo-1378-oxo-1379-oxo-1380-oxo-1381-oxo-1382-oxo-1383-oxo-1384-oxo-1385-oxo-1386-oxo-1387-oxo-1388-oxo-1389-oxo-1390-oxo-1391-oxo-1392-oxo-1393-oxo-1394-oxo-1395-oxo-1396-oxo-1397-oxo-1398-oxo-1399-oxo-1400-oxo-1401-oxo-1402-oxo-1403-oxo-1404-oxo-1405-oxo-1406-oxo-1407-oxo-1408-oxo-1409-oxo-1410-oxo-1411-oxo-1412-oxo-1413-oxo-1414-oxo-1415-oxo-1416-oxo-1417-oxo-1418-oxo-1419-oxo-1420-oxo-1421-oxo-1422-oxo-1423-oxo-1424-oxo-1425-oxo-1426-oxo-1427-oxo-1428-oxo-1429-oxo-1430-oxo-1431-oxo-1432-oxo-1433-oxo-1434-oxo-1435-oxo-1436-oxo-1437-oxo-1438-oxo-1439-oxo-1440-oxo-1441-oxo-1442-oxo-1443-oxo-1444-oxo-1445-oxo-1446-oxo-1447-oxo-1448-oxo-1449-oxo-1450-oxo-1451-oxo-1452-oxo-1453-oxo-1454-oxo-1455-oxo-1456-oxo-1457-oxo-1458-oxo-1459-oxo-1460-oxo-1461-oxo-1462-oxo-1463-oxo-1464-oxo-1465-oxo-1466-oxo-1467-oxo-1468-oxo-1469-oxo-1470-oxo-1471-oxo-1472-oxo-1473-oxo-1474-oxo-1475-oxo-1476-oxo-1477-oxo-1478-oxo-1479-oxo-1480-oxo-1481-oxo-1482-oxo-1483-oxo-1484-oxo-1485-oxo-1486-oxo-1487-oxo-1488-oxo-1489-oxo-1490-oxo-1491-oxo-1492-oxo-1493-oxo-1494-oxo-1495-oxo-1496-oxo-1497-oxo-1498-oxo-1499-oxo-1500-oxo-1501-oxo-1502-oxo-1503-oxo-1504-oxo-1505-oxo-1506-oxo-1507-oxo-1508-oxo-1509-oxo-1510-oxo-1511-oxo-1512-oxo-1513-oxo-1514-oxo-1515-oxo-1516-oxo-1517-oxo-1518-oxo-1519-oxo-1520-oxo-1521-oxo-1522-oxo-1523-oxo-1524-oxo-1525-oxo-1526-oxo-1527-oxo-1528-oxo-1529-oxo-1530-oxo-1531-oxo-1532-oxo-1533-oxo-1534-oxo-1535-oxo-1536-oxo-1537-oxo-1538-oxo-1539-oxo-1540-oxo-1541-oxo-1542-oxo-1543-oxo-1544-oxo-1545-oxo-1546-oxo-1547-oxo-1548-oxo-1549-oxo-1550-oxo-1551-oxo-1552-oxo-1553-oxo-1554-oxo-1555-oxo-1556-oxo-1557-oxo-1558-oxo-1559-oxo-1560-oxo-1561-oxo-1562-oxo-1563-oxo-1564-oxo-1565-oxo-1566-oxo-1567-oxo-1568-oxo-1569-oxo-1570-oxo-1571-oxo-1572-oxo-1573-oxo-1574-oxo-1575-oxo-1576-oxo-1577-oxo-1578-oxo-1579-oxo-1580-oxo-1581-oxo-1582-oxo-1583-oxo-1584-oxo-1585-oxo-1586-oxo-1587-oxo-1588-oxo-1589-oxo-1590-oxo-1591-oxo-1592-oxo-1593-oxo-1594-oxo-1595-oxo-1596-oxo-1597-oxo-1598-oxo-1599-oxo-1600-oxo-1601-oxo-1602-oxo-1603-oxo-1604-ox

Db 1 TGAAGGTTCGAG

RESULT 2

US-08-851-45-9

Sequence 9, Application US/08851135

Patent No. 5858674

GENERAL INFORMATION:

APPLICANT: Petros, Douglas R.

AFFILIANT: Tepland, Chris M.

TITLE OF INVENTION: METHOD FOR DETECTING PROSTATE CELLS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ernest B. Lipscomb (Bell Solitzer IP Group of

ADDRESSEE: Alison A Bird)

STREET: Post Office Drawer 44009

CITY: Charlottte

STATE: NC

COUNTRY: US

ZIP: 28244-4009

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: pc compatible

SOFTWARE: Patent In Release #1.0, Version #1.10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/851,135

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lipscomb, LLC, Ernest B.

REGISTRATION NUMBER: 24,733

PREFERENCE/INVENT NUMBER: 8143-21

TELECOMMUNICATION INFORMATION:

TELEPHONE: 704 331 6000

TELEFAX: 702 334 2014

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

FUNCTION: linear

MOLECULAR TYPE: other nucleic acid

DESCRIPTION: other "spontaneous" amino nucleotide

US-08-851-45-9

Query Match 52.4% Score 22 DB 2 Length 26

Best Local Similarity 100.0% Prod. No. 0.00038

Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 21 TGAAGTGGAGTCAAGCAAT 42

DB 1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

COMPUTER READABLE FORM:

MEDIUM TYPE: diskette, 3.5 inch, 1.44Mb storage

COMPUTER: IBM compatible pc

OPERATING SYSTEM: Windows 3.1

SOFTWARE: word perfect 6.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,902A

FILING DATE: 23-JAN-97

CLASSIFICATION: 623

PRIOR APPLICATION DATA:

AFFILIATION NUMBER: 60701310, 02/954,474

FILING DATE: 26-JAN-96, 29-SEP-92

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

FUNCTION: linear

US-08-787-902A-3

Query Match 52.4% Score 22 DB 2 Length 26

Best Local Similarity 100.0% Prod. No. 0.00048

Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 21 TGAAGTGGAGTCAAGCAAT 42

DB 1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

1 TGAAGTGGAGTCAAGCAAT 22

```

: TITLE OF INVENTION: LIPASE INHIBITORY AND COMPOSITIONS AND METHODS FOR THEIR USE
: TITLE OF INVENTION: IN ENZYMOLOGICAL HYDROLYSIS, AND PROTEIN AND GENE THERAPIES
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rhone-Poulenc Forest Inc.
: STREET: 500 Arcoia Rd. 3C43
: CITY: Collegeville
: STATE: PA
: COUNTRY: USA
: ZIP: 19426
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/985,492
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Fehner Ph.D., Paul F.
: REGISTRATION NUMBER: 35,135
: REFERENCE/DOCKET NUMBER: A2592-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610)454-3839
: TELEFAX: (610)454-3808
: INFORMATION FOR SEQ. ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 26 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "oligonucleotide"
:
: US-08-985-492-30
:
: Query Match 52.48: Score 22: DB 4: Length 26:
: Best Local Similarity 100.0%: Freq. No. 0 00038:
: Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 21 TGAAGTCGAGTCAGGATT 42
: DB 1 TGAAGTCGAGTCAGGATT 22
:
: RESULT 6
: PCT-US95-13659-5
: Sequence 5, Application PC/TUS9513659
: GENERAL INFORMATION:
: APPLICANT: Ellsner, Martin I.
: APPLICANT: Tumurtu, Mutall K.R.
: APPLICANT: Statua, Smita A.
: TITLE OF INVENTION: 3499 and 3497 Gases for H pylori and
: TITLE OF INVENTION: Polated Methods and Compositions
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NERDIE & ROSENBERG, P.C.
: STREET: 127 Peachtree Street, Suite 1200
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 303-3
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/13659
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Spratt, Gwendolyn D.

```

```

: REGISTRATION NUMBER: 36,016
: REFERENCE/DOCKET NUMBER: 2299,029
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 404/688-0770
: TELEFAX: 404/688-9880
: INFORMATION FOR SEQ. ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 26 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
:
: PCT-US95-13659-5
:
: Query Match 52.48: Score 22: DB 5: Length 26:
: Best Local Similarity 100.0%: Freq. No. 0 00038:
: Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 21 TGAAGTCGAGTCAGGATT 42
: DB 1 TGAAGTCGAGTCAGGATT 22
:
: RESULT 7
: US-08-937-063-1
: Sequence 1, Application US/08937063
: Patent No. 6187534
: GENERAL INFORMATION:
: APPLICANT: STROM, TERRY H.
: APPLICANT: VASCONCELOS, LAURO
: APPLICANT: SOUMATHIRAN, MAHIREKAM
: TITLE OF INVENTION: METHODS OF EVALUATING TRANSPLANT
: TITLE OF INVENTION: REJECTION
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HAMILTON, GREGG, SMITH & REYNOLDS
: STREET: TWO MILITARY DRIVE
: CITY: LEXINGTON
: STATE: MASSACHUSETTS
: COUNTRY: UNITED STATES
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/937,063
: FILING DATE: 24-SEP-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: GRANAMIAN, PATRICIA
: REGISTRATION NUMBER: 34,227
: REFERENCE/DOCKET NUMBER: 613697-01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (781) 861-6240
: TELEFAX: (781) 861-9540
: INFORMATION FOR SEQ. ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-937-063-1
:
: Query Match 47.68: Score 20: DB 4: Length 20:
: Best Local Similarity 100.0%: Freq. No. 0 0056:
: Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 19 GGTGAAGTCGAGTCAGG 38
: DB 1 GGTGAAGTCGAGTCAGG 20

```

RESULT 8

US-08-188-444A-13
Sequence 13, Application US/0818844A
Patent No. 5639606
GENERAL INFORMATION:
APPLICANT: Willey, James C.
TITLE OF INVENTION: Method for Quantitative Measurement of
TITLE OF INVENTOR: James C. Willey, James C. Willey
TITLE OF INVENTOR: James C. Willey, James C. Willey
NUMBER OF INVENTORS: 18
TITLE OF INVENTOR: James C. Willey, James C. Willey
ADDRESS/REFERENCE ADDRESS:
ADDRESS/REFERENCE ADDRESS:
ADDRESS/REFERENCE ADDRESS:
STREET: One Squared, Suite 1980
CITY: Toledo
STATE: Ohio
ZIP: 43604
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: pc-ats/ms-dos
SOFTWARE: Patulin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0818844A
FILING DATE: 28-Jan-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/043,390
FILING DATE: 06-Apr-1993
ATTORNEY/AGENT INFORMATION:
NAME: Martineau, Catherine R.
REGISTRATION NUMBER: 41,854
REFERENCE/AGENT NUMBER: 34265
TELEPHONE: (419) 243-1294
TELEFAX: (419) 243-8502
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: liver
PUBLICATION INFORMATION:
AUTHORS: Tokumura, K.
AUTHORS: Nakamura, Y.
AUTHORS: Sakata, K.
AUTHORS: Fujimori, K.
AUTHORS: Ohkubo, M.
AUTHORS: Sawada, K.
AUTHORS: Sakiyama, S.
TITLE: Enhanced expression of a
TITLE: glyceraldehyde-3-phosphate dehydrogenase gene in
TITLE: human lung cancers
JOURNAL: Cancer Res.
VOLUME: 47
PAGES: 5616-5619
DATE: SUMMER-1990
RELEVANT RESIDUES IN SEQ ID NO: 13: FROM 1 TO 24
US-08-188-444A-13

Query Match 42.9%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 18; Conservation 0; Mismatches 0; Indels 0;
Gaps 0.

US-08-188-444A-13

RESULT 9

US-08-876-766-13
Sequence 13, Application US/08876766
Patent No. 5876766
GENERAL INFORMATION:
APPLICANT: Willey, James C.
TITLE OF INVENTION: Method for Quantitative Measurement of
TITLE OF INVENTOR: James C. Willey, James C. Willey
TITLE OF INVENTOR: James C. Willey, James C. Willey
NUMBER OF INVENTORS: 18
TITLE OF INVENTOR: James C. Willey, James C. Willey
ADDRESS/REFERENCE ADDRESS:
ADDRESS/REFERENCE ADDRESS:
ADDRESS/REFERENCE ADDRESS:
STREET: One Squared, Suite 1980
CITY: Toledo
STATE: Ohio
ZIP: 43604
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: pc-ats/ms-dos
SOFTWARE: Patulin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/188,444
FILING DATE: 28-Jan-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/043,390
FILING DATE: 06-Apr-1993
ATTORNEY/AGENT INFORMATION:
NAME: Martineau, Catherine R.
REGISTRATION NUMBER: 41,854
REFERENCE/AGENT NUMBER: 34265
TELEPHONE: (419) 243-1294
TELEFAX: (419) 243-8502
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: liver
PUBLICATION INFORMATION:
AUTHORS: Tokumura, K.
AUTHORS: Nakamura, Y.
AUTHORS: Sakata, K.
AUTHORS: Fujimori, K.
AUTHORS: Ohkubo, M.
AUTHORS: Sawada, K.
AUTHORS: Sakiyama, S.
TITLE: Enhanced expression of a
TITLE: glyceraldehyde-3-phosphate dehydrogenase gene in
TITLE: human lung cancers
JOURNAL: Cancer Res.
VOLUME: 47
PAGES: 5616-5619
DATE: SUMMER-1990
RELEVANT RESIDUES IN SEQ ID NO: 13: FROM 1 TO 24
US-08-876-766-13

Query Match 42.9%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 18; Conservation 0; Mismatches 0; Indels 0;
Gaps 0.

US-08-876-766-13

Query Match 42.0% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No 1.2
Matches 16: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 25 GGTGAGCTGACGAGAT 42
DB 1 GGTGAGCTGACGAGAT 18

RESULT 10

US-09-156-424-5

Sequence 5, Application US/09156424
Patent No. 5948296
GENERAL INFORMATION:
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF RHOA EXPRESSION
FILE REFERENCE: PUS-0012
CURRENT APPLICATION NUMBER: US/09/156,424
CURRENT FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-156-424-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No 1.2
Matches 16: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGCTGGAGTC 34
DB 4 GGTGAAGCTGGAGTC 19

RESULT 11

US-09-213-767-5

Sequence 5, Application US/09213767
Patent No. 5948680
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
FILE REFERENCE: PUS-0024
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-213-767-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No 1.2
Matches 16: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGCTGGAGTC 34
DB 4 GGTGAAGCTGGAGTC 19

RESULT 12

US-09-205-922-5

Sequence 5, Application US/09205922
Patent No. 5951455
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G ALPHA 1 EXPRESSION

FILE REFERENCE: PUS-0020
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-205-922-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No 1.2
Matches 16: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGCTGGAGTC 34
DB 4 GGTGAAGCTGGAGTC 19

RESULT 13

US-09-205-144-5

Sequence 5, Application US/99205144
Patent No. 5958771
GENERAL INFORMATION:
APPLICANT: G. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APoptosis-2 (CIP2)
FILE REFERENCE: PUS-0021
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-205-144-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No 1.2
Matches 16: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGCTGGAGTC 34
DB 4 GGTGAAGCTGGAGTC 19

RESULT 14

US-09-205-204-5

Sequence 5, Application US/09205204
Patent No. 5958772
GENERAL INFORMATION:
APPLICANT: G. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APoptosis-2 (CIP2)
FILE REFERENCE: PUS-0020
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-205-204-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No 1.2
Matches 16: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGCTGGAGTC 34
DB 4 GGTGAAGCTGGAGTC 19

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No 1.2
Matches 16: Conservative 0 Mismatches 0 Indels 0 Gaps 0

Best Local Similarity: 100.0%; Prod. No. 1-2;
Matches: 16; conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAATTCGGAGTC 44
|||||
16 4 GGTGAAATTCGGAGTC 19

RESULT 15

US-09-212-771-5
Sequence 5, Application US/09/212771
Patent No. 698873
GENERAL INFORMATION:
APPLICANT: BOET P. MONIA
TITLE OF INVENTION: ANTISENSE REGULATION OF AKT-1 EXPRESSION
FILE REFERENCE: KIS-0044
CURRENT APPLICATION NUMBER: US/09/212771
CURRENT FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 47
SEQ ID No 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US 09-212-771-5

Query Match: 68.1%; Score 16; DB 2; Length 19;
Best Local Similarity: 100.0%; Prod. No. 1-2;
Matches: 16; conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAATTCGGAGTC 44
|||||
16 4 GGTGAAATTCGGAGTC 19

Search completed: April 18, 2003, 05:10:01
Job Time: 10:09 secs

Genome version 5.1.1.p5.1572
Copyright (c) 1993 - 2003 Computer Ltd.

OM nucleotide nucleotide search, using sw model

Run On: April 17, 2003, 20:41:01, Search time 1355 Seconds
(without alignments)
21.581 Million total updates/sec

Title: US-09-701-394-1

Perfect score: 42
1 accgatgcttgagagagagag 42

Scoring table: OLIGO.MDC
Gapop 60.0, Gapext 60.0

Searched: 653749 seqs, 50286978 residues

Word size: 0

Total number of hits satisfying chosen parameters: 377018

Minimum hit seq length: 0

Maximum hit seq length: 50

Post-processing: Listing first 45 summaries

Database: Published_Applications_NA*

- 1: /usr2/seqprod/oligo/oligo/seq1
- 2: /usr2/seqprod/oligo/oligo/seq2
- 3: /usr2/seqprod/oligo/oligo/seq3
- 4: /usr2/seqprod/oligo/oligo/seq4
- 5: /usr2/seqprod/oligo/oligo/seq5
- 6: /usr2/seqprod/oligo/oligo/seq6
- 7: /usr2/seqprod/oligo/oligo/seq7
- 8: /usr2/seqprod/oligo/oligo/seq8
- 9: /usr2/seqprod/oligo/oligo/seq9
- 10: /usr2/seqprod/oligo/oligo/seq10
- 11: /usr2/seqprod/oligo/oligo/seq11
- 12: /usr2/seqprod/oligo/oligo/seq12
- 13: /usr2/seqprod/oligo/oligo/seq13
- 14: /usr2/seqprod/oligo/oligo/seq14

Print: No. is the number of results published by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	57.1	28	4	US-09-701-394-1	Sequence 29, Appl	
2	57.1	28	4	US-09-701-394-1	Sequence 39, Appl	
3	57.1	28	4	US-09-701-394-1	Sequence 41, Appl	
4	57.1	28	4	US-09-701-394-1	Sequence 42, Appl	
5	57.1	28	4	US-09-701-394-1	Sequence 43, Appl	
6	57.1	28	4	US-09-701-394-1	Sequence 44, Appl	
7	57.1	28	4	US-09-701-394-1	Sequence 45, Appl	
8	57.1	28	4	US-09-701-394-1	Sequence 46, Appl	
9	57.1	28	4	US-09-701-394-1	Sequence 47, Appl	
10	57.1	28	4	US-09-701-394-1	Sequence 48, Appl	
11	57.1	28	4	US-09-701-394-1	Sequence 49, Appl	
12	57.1	28	4	US-09-701-394-1	Sequence 50, Appl	
13	57.1	28	4	US-09-701-394-1	Sequence 51, Appl	
14	57.1	28	4	US-09-701-394-1	Sequence 52, Appl	
15	57.1	28	4	US-09-701-394-1	Sequence 53, Appl	
16	57.1	28	4	US-09-701-394-1	Sequence 54, Appl	
17	57.1	28	4	US-09-701-394-1	Sequence 55, Appl	
18	57.1	28	4	US-09-701-394-1	Sequence 56, Appl	
19	57.1	28	4	US-09-701-394-1	Sequence 57, Appl	

20	57.1	28	4	US-09-701-394-1	Sequence 58, Appl	
21	57.1	28	4	US-09-701-394-1	Sequence 59, Appl	
22	57.1	28	4	US-09-701-394-1	Sequence 60, Appl	
23	57.1	28	4	US-09-701-394-1	Sequence 61, Appl	
24	57.1	28	4	US-09-701-394-1	Sequence 62, Appl	
25	57.1	28	4	US-09-701-394-1	Sequence 63, Appl	
26	57.1	28	4	US-09-701-394-1	Sequence 64, Appl	
27	57.1	28	4	US-09-701-394-1	Sequence 65, Appl	
28	57.1	28	4	US-09-701-394-1	Sequence 66, Appl	
29	57.1	28	4	US-09-701-394-1	Sequence 67, Appl	
30	57.1	28	4	US-09-701-394-1	Sequence 68, Appl	
31	57.1	28	4	US-09-701-394-1	Sequence 69, Appl	
32	57.1	28	4	US-09-701-394-1	Sequence 70, Appl	
33	57.1	28	4	US-09-701-394-1	Sequence 71, Appl	
34	57.1	28	4	US-09-701-394-1	Sequence 72, Appl	
35	57.1	28	4	US-09-701-394-1	Sequence 73, Appl	
36	57.1	28	4	US-09-701-394-1	Sequence 74, Appl	
37	57.1	28	4	US-09-701-394-1	Sequence 75, Appl	
38	57.1	28	4	US-09-701-394-1	Sequence 76, Appl	
39	57.1	28	4	US-09-701-394-1	Sequence 77, Appl	
40	57.1	28	4	US-09-701-394-1	Sequence 78, Appl	
41	57.1	28	4	US-09-701-394-1	Sequence 79, Appl	
42	57.1	28	4	US-09-701-394-1	Sequence 80, Appl	
43	57.1	28	4	US-09-701-394-1	Sequence 81, Appl	
44	57.1	28	4	US-09-701-394-1	Sequence 82, Appl	
45	57.1	28	4	US-09-701-394-1	Sequence 83, Appl	

ALIGNMENTS

RESULT 1	US-09-701-394-1	US-09-701-394-1
1	US-09-701-394-1	US-09-701-394-1
2	US-09-701-394-1	US-09-701-394-1
3	US-09-701-394-1	US-09-701-394-1
4	US-09-701-394-1	US-09-701-394-1
5	US-09-701-394-1	US-09-701-394-1
6	US-09-701-394-1	US-09-701-394-1
7	US-09-701-394-1	US-09-701-394-1
8	US-09-701-394-1	US-09-701-394-1
9	US-09-701-394-1	US-09-701-394-1
10	US-09-701-394-1	US-09-701-394-1
11	US-09-701-394-1	US-09-701-394-1
12	US-09-701-394-1	US-09-701-394-1
13	US-09-701-394-1	US-09-701-394-1
14	US-09-701-394-1	US-09-701-394-1
15	US-09-701-394-1	US-09-701-394-1
16	US-09-701-394-1	US-09-701-394-1
17	US-09-701-394-1	US-09-701-394-1
18	US-09-701-394-1	US-09-701-394-1
19	US-09-701-394-1	US-09-701-394-1
20	US-09-701-394-1	US-09-701-394-1
21	US-09-701-394-1	US-09-701-394-1
22	US-09-701-394-1	US-09-701-394-1
23	US-09-701-394-1	US-09-701-394-1
24	US-09-701-394-1	US-09-701-394-1
25	US-09-701-394-1	US-09-701-394-1
26	US-09-701-394-1	US-09-701-394-1
27	US-09-701-394-1	US-09-701-394-1
28	US-09-701-394-1	US-09-701-394-1
29	US-09-701-394-1	US-09-701-394-1
30	US-09-701-394-1	US-09-701-394-1
31	US-09-701-394-1	US-09-701-394-1
32	US-09-701-394-1	US-09-701-394-1
33	US-09-701-394-1	US-09-701-394-1
34	US-09-701-394-1	US-09-701-394-1
35	US-09-701-394-1	US-09-701-394-1
36	US-09-701-394-1	US-09-701-394-1
37	US-09-701-394-1	US-09-701-394-1
38	US-09-701-394-1	US-09-701-394-1
39	US-09-701-394-1	US-09-701-394-1
40	US-09-701-394-1	US-09-701-394-1
41	US-09-701-394-1	US-09-701-394-1
42	US-09-701-394-1	US-09-701-394-1
43	US-09-701-394-1	US-09-701-394-1
44	US-09-701-394-1	US-09-701-394-1
45	US-09-701-394-1	US-09-701-394-1

PRIOR APPLICATION NUMBER: 60/415,412
 PRIOR FILING DATE: 2001-08-26
 NUMBER OF SEQ ID NOS: 91
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 26
 LENGTH: 28
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-966-422B 26

Query Match: 57.1%; Score: 24; DB: 9; Length: 28;
 Best Local Similarity: 100.0%; Pred. No.: 5,76.95;
 Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAGGTGGAGTCAACGGATT 42
 DB 26 GGTGAAGGTGGAGTCAACGGATT 3

RESULT 6
 US-09-992-238-62, 63
 Sequence 62, Artificially synthesized primer sequence
 Publication No. US2003064444A1
 GENERAL INFORMATION:
 APPLICANT: BATTAGLINO, PETER
 APPLICANT: FEDER, JOHN N
 APPLICANT: MINTER, GABE
 APPLICANT: NELSON, THOMAS C
 APPLICANT: RAMANAIAHAN, CHANDRA S
 APPLICANT: WESTPHAL, RYAN
 APPLICANT: CACACE, ANGELA
 APPLICANT: BARBER, LAUREN
 APPLICANT: HARKEN, DONALD R
 APPLICANT: KOKMACKER, MICHAEL G
 TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HEPHREMB, FILE REFERENCE: 06047NP
 CURRENT APPLICATION NUMBER: US-09-992-238

PRIOR FILING DATE: 2001-11-14
 PRIOR FILING DATE: 2001-09-04
 PRIOR APPLICATION NUMBER: 60/408-86
 PRIOR FILING DATE: 2001-07-27
 PRIOR APPLICATION NUMBER: 60/268581
 PRIOR FILING DATE: 2001-02-14
 PRIOR APPLICATION NUMBER: 60/248285
 PRIOR FILING DATE: 2000-11-14
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 62
 LENGTH: 28
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: CATER FVT
 OTHER INFORMATION: Tagged(F) Ende
 US-09-992-238-62

Query Match: 57.1%; Score: 21; DB: 9; Length: 28;
 Best Local Similarity: 100.0%; Pred. No.: 5,76-05;
 Matches: 21; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAGGTGGAGTCAACGGATT 42
 DB 26 GGTGAAGGTGGAGTCAACGGATT 3

RESULT 7
 US-10-101-921-37
 Sequence 37, Application US/10101921
 Publication No. US2003064444A1
 GENERAL INFORMATION:
 APPLICANT: Nezu, Jun-ichi

APPLICANT: Ose, Asuka
 APPLICANT: Tsujii, Akira
 TITLE OF INVENTION: JPANSPORPPE GNPPE OAMP-B, C, D, AND E
 FILE REFERENCE: 06501-1040S1
 CURRENT APPLICATION NUMBER: US/10101921
 CURRENT FILING DATE: 2002-06-28
 PRIOR APPLICATION NUMBER: PCT/JP00/06416
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: JP 11/267835
 PRIOR FILING DATE: 1999-09-21
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 37
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Artificially synthesized primer sequence
 US-10-101-921-37

Query Match: 57.1%; Score: 22; DB: 9; Length: 26;
 Best Local Similarity: 100.0%; Pred. No.: 0,00087;
 Matches: 22; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 21 TGAAGGTGGAGTCAACGGATT 42
 DB 1 TGAAGGTGGAGTCAACGGATT 22

RESULT 8
 US-09-738-396-39
 Sequence 39, Application US/09738396
 Patent No. US2003029013A1
 GENERAL INFORMATION:
 APPLICANT: Reed, John C.
 APPLICANT: Giedlik, Adam
 TITLE OF INVENTION: BCL-2 Polypeptides, Encoding Nucleic Acids and Methods
 TITLE OF INVENTION: of Use
 FILE REFERENCE: P-11 4450
 CURRENT APPLICATION NUMBER: US-09-738-396
 CURRENT FILING DATE: 2000-12-14
 PRIOR APPLICATION NUMBER: US 09/461,641
 PRIOR FILING DATE: 1998-12-14
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 39
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 OTHER INFORMATION: primer
 US-09-738-396-39

Query Match: 52.4%; Score: 22; DB: 10; Length: 26;
 Best Local Similarity: 100.0%; Pred. No.: 0,00087;
 Matches: 22; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 21 TGAAGGTGGAGTCAACGGATT 42
 DB 1 TGAAGGTGGAGTCAACGGATT 22

RESULT 9
 US-09-952-604-1
 Sequence 1, Application US/09952604
 Patent No. US20020137680A1
 GENERAL INFORMATION:
 APPLICANT: Ahmed, Asif Syed
 TITLE OF INVENTION: Methods of delaying the onset of labor
 FILE REFERENCE: P-11 4450
 CURRENT APPLICATION NUMBER: US/09/952,604
 CURRENT FILING DATE: 2002-02-25

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-912-860-1

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

DB 1 TGAAGTCGAGTCGAGGATT 22

RESULT 10
 US-09-816-248-44

Sequence 44, Application US/09/816,248
 Patent No. US2002018709A1
 GENERAL INFORMATION:
 APPLICANT: BAUMANN, PETER
 APPLICANT: CECIL, THOMAS R.
 TITLE OF INVENTION: PROTECTION OF TELEMER-1 (POT-1) PROTEIN AND ENCODING
 FILE REFERENCE: 089461/0201
 CURRENT ATTORNEY NUMBER: 06,797,916,792
 CURRENT FILING DATE: 2001-03-26
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 44
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Primer
 US-09-816-248-44

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

DB 1 TGAAGTCGAGTCGAGGATT 22

RESULT 11
 US-09-992-860-1

Sequence 1, Application US/09/992,860
 Patent No. US2002014472A1
 GENERAL INFORMATION:
 APPLICANT: chen, Kuang Yu
 APPLICANT: Ho, Chi Tang
 APPLICANT: Rosen, Robert E.
 APPLICANT: Ghali, Goshka
 TITLE OF INVENTION: Black Tea Extract for Prevention of Disease
 FILE REFERENCE: 00-0173
 CURRENT ATTORNEY NUMBER: 06,797,916,860
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/248,942
 PRIOR FILING DATE: 2000-11-15
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 1
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-912-860-1

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

DB 1 TGAAGTCGAGTCGAGGATT 22

RESULT 12
 US-09-918-702-38

Sequence 38, Application US/09/918,702
 Patent No. US2002014667B1
 GENERAL INFORMATION:
 APPLICANT: Benvenisty, Nissim
 TITLE OF INVENTION: Directed Differentiation of Embryonic Stem
 FILE REFERENCE: 1822/114
 CURRENT ATTORNEY NUMBER: 06,797,916,792
 CURRENT FILING DATE: 2001-07-31
 NUMBER OF SEQ ID NOS: 74
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 38
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 CIRCLE INFORMATION: 5' End of 3'-phosphatidyl-4-phosphate
 OTHER INFORMATION: dehydrogenase
 US-09-918-702-38

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

DB 1 TGAAGTCGAGTCGAGGATT 22

RESULT 13
 US-09-777-742-1

Sequence 1, Application US/09/777,742
 Patent No. US2002014235A1
 GENERAL INFORMATION:
 APPLICANT: Avihasson, Yinyos
 APPLICANT: Ma, Nall
 APPLICANT: Strom, Terry
 APPLICANT: Soares, Miguel C.
 APPLICANT: Ferraz, Christian
 APPLICANT: Meikham, Subhathiran
 TITLE OF INVENTION: MEASUREMENT OF PROTECTIVE GATES IN ALGAE REPRODUCTION
 FILE REFERENCE: 01948-050001
 CURRENT ATTORNEY NUMBER: 06,797,777,742
 CURRENT FILING DATE: 2001-02-06
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetically generated primer
 US-09-777-742-1

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.0181;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

DB 1 GTGAAGTCGAGTCGAGGATT 48

RESULT 14
 US-09-777-742-1

Sequence 1, Application US/09/777,742
 Patent No. US2002014235A1
 GENERAL INFORMATION:
 APPLICANT: Avihasson, Yinyos
 APPLICANT: Ma, Nall
 APPLICANT: Strom, Terry
 APPLICANT: Soares, Miguel C.
 APPLICANT: Ferraz, Christian
 APPLICANT: Meikham, Subhathiran
 TITLE OF INVENTION: MEASUREMENT OF PROTECTIVE GATES IN ALGAE REPRODUCTION
 FILE REFERENCE: 01948-050001
 CURRENT ATTORNEY NUMBER: 06,797,777,742
 CURRENT FILING DATE: 2001-02-06
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetically generated primer
 US-09-777-742-1

Db 1 GGTGAAGTCTGGAGTCAACG 20

RESULT 14

US-09-899-569A-36

Sequence 36, Application US/09899569A

Patent No. US20020142003A1

GENERAL INFORMATION:

APPLICANT: No. US79026142003Albert Schweitzer

APPLICANT: Marwa Scherl Mostager

APPLICANT: Wolfgang Sommergruber

APPLICANT: Roger Abseher

TITLE OF INVENTION: Tumorssoziliertes Antigen (B345)

FILE REFERENCE: 0652, 2280001

CURRENT APPLICATION NUMBER: US/09/899, 569A

CURRENT FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: DE 100 33 080 0

PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: DE 101 19 294 0

PRIOR FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 60/243,158

PRIOR FILING DATE: 2000-10-25

PRIOR APPLICATION NUMBER: US 60/297,747

PRIOR FILING DATE: 2001-06-14

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 36

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE: Artificial sequence

OTHER INFORMATION: Description of the artificial sequence: Primer

US-09-899-569A-36

Query Match

Best Local Similarity: 47.6%; Score 20; DB 10; Length 22;

Matches: 20; Gaps: 0; Mismatches: 0; Trunc: 0; Cuts: 0;

Db 19 GGTGAAGTCTGGAGTCAACG 38

Db 3 GGTGAAGTCTGGAGTCAACG 22

RESULT 15

US-09-897-412-4

Sequence 4, Application US/09897412

Patent No. US20020142956A1

GENERAL INFORMATION:

APPLICANT: Davis, Richard J

APPLICANT: Page, Keith J

TITLE OF INVENTION: Use of Secretin Receptor Ligands in Treatment of Cystic

TITLE OF INVENTION: Fibrosis (CF) and Chronic Obstructive Pulmonary Disease

FILE REFERENCE: 620-148

CURRENT APPLICATION NUMBER: US/09/897,412

CURRENT FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: GB 0016441.8

PRIOR FILING DATE: 2000-07-04

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-897-412-4

Query Match

Best Local Similarity: 45.2%; Score 19; DB 10; Length 22;

Matches: 19; Gaps: 0; Mismatches: 0; Trunc: 0; Cuts: 0;

QY 19 GGTGAAGTCTGGAGTCAAC 37

Db 4 GGTGAAGTCTGGAGTCAAC 22

Search completed: April 18, 2003, 21:46:40
Job time: 1956 secs

4

5

Best Local Similarity: 100.0%; Prod. No. 0.0012;
Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAGTGGAGTCAAGCAAT 42
|||||
ID 26 GGTGAAGTGGAGTCAAGCAAT 4

RESULT 8

US-09-992-782A-4476

Sequence: 33; Application: US/09992782A

GENERAL INFORMATION:

APPLICANT: Battaglini, P.

APPLICANT: Feder, J. N.

APPLICANT: Mintoff, G.

APPLICANT: Ramanathan, C. S.

APPLICANT: Westphal, R.

APPLICANT: Harker, D. R.

APPLICANT: Targoff, A.

APPLICANT: Barber, L.

APPLICANT: Kornacker, M. G.

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRM7,

TITLE OF INVENTION: EXPRESSED HIGHLY IN SPINAL CORD

FILE REFERENCE: 10044ND

CURRENT APPLICATION NUMBER: US/09992782A

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/245,731

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/266,590

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/417,121

PRIOR FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PatGen Ver. 2.1

SEQ ID NO: 42

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CAPRI PVIC

US-09-992-782A-44

Query Match: 57.1%; Score: 24; 18 47; Length: 28;

Best Local Similarity: 100.0%; Prod. No. 0.0012;

Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAGTGGAGTCAAGCAAT 42
|||||

ID 26 GGTGAAGTGGAGTCAAGCAAT 4

RESULT 9

US-09-992-238-6276

Sequence: 62; Application: US/09992238

GENERAL INFORMATION:

APPLICANT: Battaglini, PETER

APPLICANT: Feder, JOHN N

APPLICANT: MINIER, GABE

APPLICANT: NELSON, THOMAS G

APPLICANT: RAMANATHAN, CHANDRA S

APPLICANT: WESTPHAL, RYAN

APPLICANT: CARACE, ANGELA

APPLICANT: BARKER, LAGREN

APPLICANT: HARKEN, DONALD R

APPLICANT: KORNACKER, MICHAEL G

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRM8,

TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN

FILE REFERENCE: 10044ND

CURRENT APPLICATION NUMBER: US/09992238

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/271166

PRIOR FILING DATE: 2001-09-04

PRIOR APPLICATION NUMBER: 60/308285

PRIOR FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/268581

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/248285

PRIOR FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatGen Ver. 2.1

SEQ ID NO: 62

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CAPRI PVIC

US-09-992-238-62

Query Match: 57.1%; Score: 24; 18 47; Length: 28;

Best Local Similarity: 100.0%; Prod. No. 0.0012;

Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAGTGGAGTCAAGCAAT 42
|||||

ID 26 GGTGAAGTGGAGTCAAGCAAT 4

RESULT 10

US-09-992-341-4176

Sequence: 41; Application: US/09992341

GENERAL INFORMATION:

APPLICANT: FEDER, JOHN N.

APPLICANT: MINIER, GABE

APPLICANT: RAMANATHAN, CHANDRA S.

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRM9,

TITLE OF INVENTION: EXPRESSED IN SKIN IN TIGHTLY CLUSTERS AND IN OTHER EPITHELIAL CELLS

FILE REFERENCE: 10048ND

CURRENT APPLICATION NUMBER: US/09992341

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/408,540

PRIOR FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/261,782

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: 60/248,484

PRIOR FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatGen Ver. 2.1

SEQ ID NO: 41

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CAPRI PVIC

US-09-992-341-41

Query Match: 57.1%; Score: 24; 18 47; Length: 28;

Best Local Similarity: 100.0%; Prod. No. 0.0012;

Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAGTGGAGTCAAGCAAT 42
|||||

ID 26 GGTGAAGTGGAGTCAAGCAAT 4

RESULT 11

US-10-120-604-18476

Sequence: 184; Application: US/10120604

GENERAL INFORMATION:

APPLICANT: Bristol Myers Squibb Company

TITLE OF INVENTION: PEPTIDES THAT ENCODE THE TWO N-TERM HUMAN 1 PROTEIN COUPLED RECEPTOR

TITLE OF INVENTION: HGPGRM24 AND HGPGRM25, AND OTHER VARIANTS THEREOF

Mon Apr 21 08:33:23 2003

us-09-701-394-1.rmpm

Page 6

Search completed: April 18, 2003, 18:43:58
Index time: 48820 secs


```

1 CURRENT FILING DATE: 2002-10-11
2 PRIOR APPLICATION NUMBER: U.S. 60/328,479
3 PRIOR FILING DATE: 2001-10-11
4 NUMBER OF SEQ. ID NOS: 96
5 SOFTWARE: Patent In version 4.1
6 SEQ. ID NO: 97
7 LENGTH: 28
8 TYPE: DNA
9 ORGANISM: Homo sapiens
10-10-078-93

```

```

Query Match 57.1% Score 243 DB 97 Length 283
Best Local Similarity 100.0% Prod. No. 0.000457
Matches 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

```

QY 19 GGTGAAGTGGAGTCAGACGACAT 42
ID 26 GGTGAAGTGGAGTCAGACGACAT 4

```

```

RESULT 4
US-10-423-412-29/7
1 Sequence 29, Application US/10423412
2 GENERAL INFORMATION:
3 APPLICANT: Bristol-Myers Squibb Company
4 TITLE OF INVENTION: REVEL HUMAN G PROTEIN COUPLED RECEPTOR, HEPHRAMY4, AND METHODS OF
5 FILE REFERENCE: 100330A CIP
6 CURRENT APPLICATION NUMBER: US/10/323,412
7 PRIOR FILING DATE: 2002-12-18
8 PRIOR APPLICATION NUMBER: U.S. 09/964,459
9 PRIOR FILING DATE: 2001-09-26
10 PRIOR APPLICATION NUMBER: U.S. 60/245,833
11 PRIOR FILING DATE: 2000-09-27
12 PRIOR APPLICATION NUMBER: U.S. 60/261,776
13 PRIOR FILING DATE: 2001-01-16
14 PRIOR APPLICATION NUMBER: U.S. 60/405,451
15 PRIOR FILING DATE: 2001-07-14
16 PRIOR APPLICATION NUMBER: U.S. 60/413,202
17 PRIOR FILING DATE: 2001-08-17
18 NUMBER OF SEQ. ID NOS: 69
19 SOFTWARE: Patent In version 4.1
20 SEQ. ID NO: 29
21 LENGTH: 28
22 TYPE: DNA
23 ORGANISM: Homo sapiens
24-10-423-412-29

```

```

Query Match 57.1% Score 243 DB 97 Length 283
Best Local Similarity 100.0% Prod. No. 0.000457
Matches 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0
QY 19 GGTGAAGTGGAGTCAGACGACAT 42
ID 26 GGTGAAGTGGAGTCAGACGACAT 4

```

```

RESULT 4
US-10-423-412-26/7
1 Sequence 26, Application US/10423412
2 GENERAL INFORMATION:
3 APPLICANT: Bristol-Myers Squibb Company
4 TITLE OF INVENTION: REVEL HUMAN G PROTEIN COUPLED RECEPTOR, HEPHRAMY4
5 FILE REFERENCE: 10044 CIP
6 CURRENT APPLICATION NUMBER: US/10/323,412
7 PRIOR FILING DATE: 2002-09-27
8 PRIOR APPLICATION NUMBER: U.S. 09/966,422
9 PRIOR FILING DATE: 2001-09-26
10 NUMBER OF SEQ. ID NOS: 91
11 SOFTWARE: Patent In version 4.2
12 SEQ. ID NO: 26
13 LENGTH: 28
14 TYPE: DNA

```

```

1 ORGANISM: Homo sapiens
2 US-10-262-272A-26

```

```

Query Match 57.1% Score 243 DB 97 Length 283
Best Local Similarity 100.0% Prod. No. 0.000457
Matches 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

```

QY 19 GGTGAAGTGGAGTCAGACGACAT 42
ID 26 GGTGAAGTGGAGTCAGACGACAT 4

```

```

RESULT 5
US-10-348-119-795/76
1 Sequence 795, Application US/10348119
2 GENERAL INFORMATION:
3 APPLICANT: Bristol-Myers Squibb Company
4 TITLE OF INVENTION: IDENTIFICATION OF POLYPEPTIDES AND POLYPEPTIDE FOR PROTEIN
5 TITLE OF INVENTION: ACTIVITY OF PROTEIN THAT INTERACT WITH PROTEIN TYROSINE KIN
6 FILE REFERENCE: 100185 NP
7 CURRENT APPLICATION NUMBER: US/10/348,119
8 PRIOR FILING DATE: 2004-01-17
9 PRIOR APPLICATION NUMBER: US 60/450,061
10 PRIOR FILING DATE: 2002-01-18
11 NUMBER OF SEQ. ID NOS: 795
12 SOFTWARE: Patent In version 4.2
13 SEQ. ID NO: 795
14 LENGTH: 28
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 US-10-348-119-795

```

```

Query Match 57.1% Score 243 DB 97 Length 283
Best Local Similarity 100.0% Prod. No. 0.000457
Matches 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0
QY 19 GGTGAAGTGGAGTCAGACGACAT 42
ID 26 GGTGAAGTGGAGTCAGACGACAT 4

```

```

RESULT 6
US-60-446-655-42/C
1 Sequence 32, Application US/60446655
2 GENERAL INFORMATION:
3 APPLICANT: Bristol-Myers Squibb Company
4 TITLE OF INVENTION: REVEL HUMAN G PROTEIN COUPLED RECEPTOR
5 FILE REFERENCE: 100286 PSP
6 CURRENT APPLICATION NUMBER: US/60/446,655
7 PRIOR FILING DATE: 2004-02-11
8 NUMBER OF SEQ. ID NOS: 112
9 SOFTWARE: Patent In version 4.2
10 SEQ. ID NO: 32
11 LENGTH: 28
12 TYPE: DNA
13 ORGANISM: Artificial
14 FEATURE:
15 OTHER INFORMATION: oligonucleotide
16 US-60-446-655-42

```

```

Query Match 57.1% Score 243 DB 97 Length 283
Best Local Similarity 100.0% Prod. No. 0.000457
Matches 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

```

QY 19 GGTGAAGTGGAGTCAGACGACAT 42
ID 26 GGTGAAGTGGAGTCAGACGACAT 4

```

```

RESULT 7
US-10-501-439-1A-1

```

```

: Sequence 1: Application PC/US0143931A
: GENERAL INFORMATION:
: APPLICANT: Chen, Kuang Yu
: APPLICANT: Ho, Chi-Tang
: APPLICANT: Rosen, Robert T.
: APPLICANT: Chai, Geetha
: APPLICANT: Rutgers, the State University
: TITLE OF INVENTION: Black Tea Extract for Prevention of Disease
: FILE REFERENCE: RU-0172
: CURRENT APPLICATION NUMBER: PC/US0143931A
: CURRENT FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: 467948, 942
: PRIOR FILING DATE: 2000-11-15
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 1
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: PCT-US01-43931A-1

```

```

Query Match          52.4%, Score 22: DB 1: Length 26,
Best Local Similarity 100.0%, Pred. No. 0.0063:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 TGAAGTGGAGTCAACGGATT 42
DB 1 TGAAGTGGAGTCAACGGATT 22

```

```

RESULT 8
US-09-738-396A-39
: Sequence 39: Application US/09/48496A
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Godzik, Adam
: TITLE OF INVENTION: p1-C Polypeptides, Encoding Nucleic Acids and Methods
: TITLE OF INVENTION: of use
: FILE REFERENCE: P-11 4450
: CURRENT APPLICATION NUMBER: US/09/738, 396A
: CURRENT FILING DATE: 2000-12-14
: PRIOR APPLICATION NUMBER: US 09/461,641
: PRIOR FILING DATE: 1999-12-14
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 39
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: primer
: US-09-738-396A-39

```

```

Query Match          52.4%, Score 22: DB 7: Length 26,
Best Local Similarity 100.0%, Pred. No. 0.0063:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 TGAAGTGGAGTCAACGGATT 42
DB 1 TGAAGTGGAGTCAACGGATT 22

```

```

RESULT 9
US-10-275-172-5
: Sequence 5: Application US/10275172
: GENERAL INFORMATION:
: APPLICANT: Merck Patent GmbH
: TITLE OF INVENTION: New Threonine-serine kinase (Htsk1)
: FILE REFERENCE: htsk1bws
: CURRENT APPLICATION NUMBER: US/10/275,172

```

```

: CURRENT FILING DATE: 2002-11-04
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 5
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: primer 3
: US-10-275-172-5

```

```

Query Match          52.4%, Score 22: DB 9: Length 26,
Best Local Similarity 100.0%, Pred. No. 0.0063:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 TGAAGTGGAGTCAACGGATT 42
DB 1 TGAAGTGGAGTCAACGGATT 22

```

```

RESULT 10
US-10-275-556-5
: Sequence 5: Application US/10275556
: GENERAL INFORMATION:
: APPLICANT: Merck Patent GmbH
: TITLE OF INVENTION: Serine-threonine kinase 3 (Htsk-3)
: FILE REFERENCE: htsk3bws
: CURRENT APPLICATION NUMBER: US/10/275,556
: CURRENT FILING DATE: 2002-11-07
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 5
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: primer 4
: US-10-275-556-5

```

```

Query Match          52.4%, Score 22: DB 9: Length 26,
Best Local Similarity 100.0%, Pred. No. 0.0063:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 TGAAGTGGAGTCAACGGATT 42
DB 1 TGAAGTGGAGTCAACGGATT 22

```

```

RESULT 11
US-60-434-165-26
: Sequence 26: Application US/60434165
: GENERAL INFORMATION:
: APPLICANT: Malzok, Martin M.
: APPLICANT: Wu, Xuemai
: APPLICANT: Wang, Pei
: APPLICANT: Bai, Yuchen
: TITLE OF INVENTION: Contrastive targets
: FILE REFERENCE: poly25054
: CURRENT APPLICATION NUMBER: US-60-434,165
: CURRENT FILING DATE: 2002-12-17
: PRIOR APPLICATION NUMBER: US 03/844,864
: PRIOR FILING DATE: 2001-04-27
: PRIOR APPLICATION NUMBER: US 60/411,262
: PRIOR FILING DATE: 2002-09-17
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: Patent In version 3.1
: SEQ ID NO 26
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Human
: US-60-434-165-26

```

```

Query Match          52.1%, Score 22: DB 11: Length 26,

```

Best Local Similarity 100.0%: Pred. No. 0.0063;
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTCGAGTCACGAGATT 42

DB 1 TGAAGTCGAGTCACGAGATT 22

RESULT 12

US-60-44-761-26

Sequence 26: Application US/6044761

GENERAL INFORMATION:

APPLICANT: Matzok, Martin M.

APPLICANT: Wu, Xiumei

APPLICANT: Wang, Yuchou

TITLE OF INVENTION: Control Effective Targets

FILE REFERENCE: P01925055

CURRENT APPLICATION NUMBER: US/6044761

PRIOR FILING DATE: 2004-01-14

PRIOR APPLICATION NUMBER: US 09/2944,864

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: US 09/244,355

PRIOR FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: US 09/411,372

PRIOR FILING DATE: 2002-09-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 4.1

SEQ ID No 26

LENGTH: 26

TYPE: DNA

ORGANISM: Human

US-60-44-761-26

Query Match 52.4%: Score 22: DB 11: Length 26:

Best Local Similarity 100.0%: Pred. No. 0.0063;

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTCGAGTCACGAGATT 42

DB 1 TGAAGTCGAGTCACGAGATT 22

RESULT 13

US-60-44-2164-26

Sequence 26: Application US/60442164

GENERAL INFORMATION:

APPLICANT: Matzok, Martin M.

APPLICANT: Wu, Xiumei

APPLICANT: Wang, Yuchou

TITLE OF INVENTION: Control Effective Targets

FILE REFERENCE: P01925056

CURRENT APPLICATION NUMBER: US/60442164

PRIOR FILING DATE: 2003-01-24

PRIOR APPLICATION NUMBER: US 09/244,864

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: US 60/444,165

PRIOR FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: US 60/411,372

PRIOR FILING DATE: 2002-09-17

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 4.1

SEQ ID No 26

LENGTH: 26

TYPE: DNA

ORGANISM: Human

US-60-44-2164-26

Query Match 52.4%: Score 22: DB 11: Length 26:

Best Local Similarity 100.0%: Pred. No. 0.0063;

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTCGAGTCACGAGATT 42

DB 1 TGAAGTCGAGTCACGAGATT 22

RESULT 14

US-09-778-0143-1

Sequence 1: Application US/09778013

GENERAL INFORMATION:

APPLICANT: Strom, Terry B.

APPLICANT: Subhadhiran, Manikam

TITLE OF INVENTION: METHOD OF EVALUATING TRANSMISSION

FILE REFERENCE: 01948-061001

CURRENT APPLICATION NUMBER: US 09/778,013

PRIOR FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US 09/778,013

PRIOR FILING DATE: 2003-01-24

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

Mon Apr 21 08:33:24 2003

us-09-701-394-1.rnpn

Page 5

|||||
Db 1 GGTGAAGCTGGAGTCAAG 20

Search completed: April 18, 2003, 21:13:51
Job time : 8979 secs

1
2
3